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GENERAL INFORMATION:
APPLICANT: Payne, Jewel M.
APPLICANT: Payne, Jewel M.
APPLICANT: Payne, Jewel M.
APPLICANT: Bagley, Angele D.
TITLE OF INVENTION: No. 5262158el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                   Sequence 3
Sequence 4
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CIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/876,280

FILING DATE: 19920430

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: SAliwanchik, David R.

REGISTRATION NUMBER: 31,794

REDERENCE/DOCKET NUMBER: 31,794

RELEPHONE: 904-375-8100

TELEFRAK: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
CLONE: B. coli NM522(pMYC2120) NRRL B-18769
US-07-876-280-30
                 US-07-951-715A-7
US-08-459-448A-7
US-08-459-55A-7
US-08-459-504B-7
US-08-459-444-7
US-08-547-42-7
US-09-547-42-7
US-08-961-803-9
US-09-661-322A-63
US-09-661-322A-63
US-09-661-322A-38
US-09-661-322A-38
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                                                                                                                                                               -07-973-320-4
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                                                                                                                                                                                                                                                        Sequence 30, Application US/07876280 Patent No. 5262158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 1157 amino acids TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein HYPOTHETICAL: YES ANTI-SENSE: NO ORIGINAL SOURCE:
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CITY: Gai
STATE: FI
COUNTRY:
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US-07-876-280-30
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3: /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2 6/ptodata/2/iaa/PCTUS COMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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LIBRARY: Lambdagem (TM)
LIBRARY: FONCERRADA
CLONE: 50C
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                                            1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                        14;
    Length 1157;
tch 66.3%; Score 4007; DB 1; Length 1 al Similarity 66.1%; Pred. No. 2.3e-285; 773; Conservative 144; Mismatches 238; Indels
 Query Match
Best Local S
Matches 773
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Sequence 2, Application US/07812180A
Patent No. 5366892
GENERAL INFORMATION:
APPLICANT: Foncerrada, Luis R
APPLICANT: Fayne, Jewel M
APPLICANT: Faick, August J
TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding TITLE OF INVENTION: thuringiensis Isolate and a No. 5366892el Gene Encoding NUMBER OF SEQUENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENTION: Coleopteran-Active Toxin
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                                                   1009 RLOOAWNLYDORNAIPNGDFRNGLSNWNATPGVEVQOINHTSVLVIPNWDEQVSQOFTVQ
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STATE: EL
COUNTRY: Gainesville
STATE: TL
COUNTRY: USA
ZIP: 32606
COMPUTER: EL
COUNTRY: USA
ZIP: 32606
COMPUTER: FLORDY disk
COMPUTER: EL PR PC COMPATIBLE
COMPUTER: EL PR PC COMPATIBLE
COMPUTER: EL PR PC COMPATIBLE
COMPUTER: IBP PC COMPATIBLE
COMPUTER: IBP PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CUREASIPTOMION DATA:
APPLICATION NAME: US/07/812,180A
FILING DATE: 19920102
CILASSIPTCATION: 435
ATTORNBY/AGENT INFORMATION:
TELEPHONE: 904-375-8100
TE
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Best Local Similarity 66.1%; Pred. No. 2.3e-285;
Matches 773; Conservative 144; Mismatches 238;
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STREET: 2421 N.W. 41st Street, Ste
CITX: Gainesville
1019
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ETFISSSTVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLMPSSTVSVWEMIMKQVED 120
                                                                                                                                                                                                                                                                                                 ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PSSOC
IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11 LIBRARY OF LUIS I
CLONE: 50C(a)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1093
FILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
REGISTRANICH/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION: 1NFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELRFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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STRANDEDNESS: single
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                                                                          AKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240.
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    SIPSFAVSGHEVLLLAVYAQAVNIHLLLLRDASIFGEEWGFTPGEISRFYNRQVQLTAB
                                                                                                                                                                                         241 YSDYCVKWYKIGLDKLKGTISKSWLNYHQPRREWTLLVLDLVALPPNYDTHMYPIETTAQ
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                                                            LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
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14; Query March

66.3%; Score 4007; DB 1; Length 1157;
Best Local Similarity 66.1%; Pred. No. 2.36-285;
Matches 773; Conservative 144; Mismatches 238; Indels 14 GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT:

APPLICANT: FONCERRADA

Mon Jun

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1129 PYTDQMWIEISETEGTFYIESVELIVDVE 1157
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TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                   US-07-941-650A-2
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241 YSDYCVKWYKIGLDKLKGTTSKSWLNYHQFRREWTLLVLDLVALFPNYDTHMYPIETTAQ 300
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                                                    SIPSFAVSGHEVILLAVYAQAVNLHILLLRDASIFGEEMGFTPGEISRFYNRQVQLTAE
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                                                                            APPLICANT: Uyeda, Kendrick A. APPLICANT: Uyeda, Kendrick A. APPLICANT: Bradfisch, Gregory A. TITLE OF INVENTION: Process for Controlling Lepidopteran Pests NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1157;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/941,650A
FILING DATE: 19920908
CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-SEP-1991
PRIOR APPLICATION NUMBER: US 07/758,935
FILING DATE: 12-SEP-1991
PRIOR APPLICATION NUMBER: US 07/658,935
FILING DATE: 11-FEB-1991
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/642,112
FILING DATE: 16-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: SA11,wanchik, David R.

REGISTRATION NUMBER: US 07/642,112
ATTORNEY/AGENT INFORMATION:
NAME: SA11,wanchik, David R.

REGISTRATION NUMBER: US 07/642,112
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Best Local Similarity 66.1%; Pred. No. 2.3e-285;
Matches 773; Conservative 144; Mismatches 238;
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I IMMEDIATE SOURCE: PSSOC
I CLOONE: E. coli NMS22(pMYC1638), NRRL B-18751
US-07-941-650A-2
                                                                                                                                                                    ...ureSSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite i
CITY: Gainesville
STATE: FL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/07941650A
Patent No. 6294184
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                                       SIPSFAVSGHEVLLLAVYAQAVNLHLLLLRDASIFGEEWGFTPGEISRFYNRQVQLTAE
                                                                                                                                         LPLNNTEYLEYWGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD
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RESULT 5

21; 180 VAKIPSFAISGQEVPILSVYAQAANLHILLIRDASIFGAEWGFTPGEISTFYDRQVTRTA 239
181 RINMGSFSQTNYETPILPTYAQAASIHILVMRDVQIYGKEWGYPQNDIDLFYKEQVSYTA 240 DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179 QLTREVYTDPIVPNRETSGGFCRRWSLN----SDI-----SFSEVESAVIRSPHLFDIL 349 :||||::||||: ELTREIFTDPV-----GSYVIGGSSTLISWYDMIPAALPSFSTLEN-LLRKPDFFTLL 352 9 9 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP 61 ETFISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVE APPLICANT: Obba, Michio
APPLICANT: Obba, Michio
APPLICANT: Sato, Rejichi
APPLICANT: Sato, Rejichi
APPLICANT: Satonaki, No. 5359048ukazu
APPLICANT: Gyiwara, Katsutoshi
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Hori, Shouji
APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5359048el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS: DB 1; Length 1149; COUNTKI: US
ZIP: 32606
COMPUTER EALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELA PE COMPATIBLE
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,203
FILING DATE: 19920723
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: 31,794
REPE Query Match 60.6%; Score 3662.5; DB 1; Best Local Similarity 63.8%; Pred. No. 4.6e-260; Matches 752; Conservative 109; Mismatches 257; ADDRESSEE: David R. Saliwanchik STREET: 2411 N.W. 41st Street, Suite CITY: Gainesville STATE: FL COUNTRY: US Sequence 2, Application US/07915203 Patent No. 5359048 MOLECULE TYPE: protein AMINO ACID linear TOPOLOGY: ; MOLECULE T US-07-915-203-2 120 300 301 ઠે 셤

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NUMBER OF SEQUENCES
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                                                                       747 GWTGSTGIEVVEGDVLFKORSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFI
                                 353 QEIRMYTS---FRQNGTIEYYNYWGGQRLTLSYIYGSSF--NKYSGVLAGAEDIIPVGQN
                                                                                                      469 ID---EIPPENEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVY
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APPLICANT: Iwahana, Hidenori
APPLICANT: Sato, Relichi
APPLICANT: Sato, Relichi
APPLICANT: Ogiwara, Katsutoshi
APPLICANT: Sakanaka, Katsutoshi
APPLICANT: Hori, Hidetaki
APPLICANT: Hori, Hidetaki
APPLICANT: Asano, Shouji
APPLICANT: Rawasugi, Tadaaki
TITLE OF INVENTION: No. 5747450el Microorganism and Insecticide
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Patent No. 5747450
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APPLICANT: INAMANA,
APPLICANT: Sato, Re
APPLICANT: Suzuki,
APPLICANT: Ogiwara,
APPLICANT: Ogiwara,
APPLICANT: Hand
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                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-UTL-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/915,203
FILING DATE: 33-UTL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1149 amino acids
                                                                                    STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d.
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                                                                    Gainesville
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             283366 segs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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S49247

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JUC2211

JUC221

JUC221
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
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Sequence:
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USBS81 139870	A26858	I40590	139815	S25383	139814	A22798	504181	139811	S10228	A27323	B29838	JH0261	JC7140	B42459
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1136	1180	719	719	719	719	934	823	652	629	652	934	649	655	380
30.9	9.3	28.7	28.5	28.4	28.3	27.9	23.4	21.1	20.8	20.6	18.7	18.5	17.7	17.6
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1868.5 30 1778.5 29				1713.5	1707.5	1683.5	1413	1272.5	1258.5	1245	1132.5	1116.5	1069.5	1061

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RESULT 1 140589 parasporal crystal protein cry8Cal - Bacillus parasporal crystal protein cry8Cal - Bacillus N;Alternate names: parasporal crystal protein C;Species: Bacillus thuringlensis C;Date: 12-Aug-1996 #sequence_revision 12-Aug C;Accession: 140589 R;Sato, R.; Takeuchi, K.; Ogiwara, K.; Minami Curr. Microbiol. 28, 15-19, 1994 A;Title: Cloning, heterologous expression, ar A;Reference number: 140589 A;Accession: 140589 A;Status: preliminary; translated from GB/EME A;Molecule type: DNA A;Residues: 1-1160 exEs> C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin	1 Dral cr. test and cr. test and cr. 12-Au 13-Au 14-Crobin rence n ssion: 13: pre- 13: pre- 13: pre- 14: pre- 15: pre- 16: pre- 17: pre- 18:	crystal names: Aug-1996 Aug-1996 Takeuch piol, biol, 140589 relimina rrype: 1140589 I-1160 erences: ly: para	protein cr pharasporal thuringie; #sequence i, K.; Ogie; i, 15-19, 11 leterologou 140589; M Iry; transl, rry; transl, RRS. EMBL: U043 eporal cry	in cr poral ingle ingle ingle iogou logou ransl	cry8cal al crys ce_revis ce_revis giwara, 1994 nous exp MUID:9 slated	A all - all - systal - all - a	:s thuringiensis cryIII 1-1996 #text_chan r. M.; Kaji, Y.; d localization o IID:7764305 sL/DDBJ	ge 01-Dec-2000 Suzuki, N.; Hori, H.; Asar f a novel crystal protein ; PID:g532524
Query Best Matc)	Query Match Best Local S Matches 767	ch 1 Similarity 64.2%; 767; Conservative 1	rity	61. 64. ative	28;	SC PT 1993	Score 3733.5; DB 2; Length Pred. No. 1.6e-208; 9; Mismatches 257; Indels	11160; 61; Gaps 21;
8 8			ONEYE ONEYE	ILDAS.	SST.	SVSDN SVSDN	MSPANQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQARAYKDYLRMSEGENPELFGNP 	ISEGENPELFGNP 60
& 4	61		S-STV	Ordic	IVG - IVS	QVLGA: TIISG	ETPISS-STVOTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLMPSSTVSVWEMIMKQVB	.VSVWEMIMKQVB 119
S G	120		KITDS KILDS	VRKTA VRSRA	EAG HAD	LOGLG LANSR	DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKOWLENRNDTRARSVVVTQYIALBLDF 	VVTQYIALELDF 179
ò a	180		SFAIS ::	GOEVP NYETP	ELLS.	VYAQA TYAQA	VAKIPSFAISGGEVPLLSVYAQAANLHLLLEDASIFGAEWGFTFGRISTFYDRQVIRTA 	STEYDRQVTRTA
ò a	240		CVKNY :	NTGLD - : NAGLN	ÄTK KR:: K	GTNAA GTGAK	QYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYFIETTA 	NDTRTYPIETTA 299 : NDARIYPLETNA 300
oy D	300		OLTREVYTOPI :: : ELTREIFTOPV	IVENR:	ETS.	GGFCR : GSYVT	QLTREVYIDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDIL : :	-SFSEVESAVIRSPHLFDIL 349 : : : : PSFSTLEN-ILRKFDFFTLL 352
ò a	350	-	YTTRA(: YTS	GLPLN - FRON	- FA ETE	EYLEY 	SEIEFYTTRAGLPLANT-EYLBYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANK 	TSNKIKYYDLANK 408 : AGAEDIIPVGQN 407
ò	409		RSLGA	DLANY	YAQ	VYGVP	DIFQVRSLGADLANYYAQVYGVPYASFTILLDKNTGSGSVGGFTYSKPHTIMQVCTQNYNT	ITIMQVCTQNYNT 468

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paragoral crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis
N;Alternate names: parasporal crystal protein cryA4
(Species: Bacillus thuringiensis subsp. thuringiensis
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000
C;Accession: 500873
(Shizard, B.L.; Whiteley, H.K.)
Nucleic Acids Res. 16, 2723-2724, 1988
A;Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus
A;Reference number: 500873; MUID:88203216; PMID:3362680
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                                                                                 AKKAVNGLFTSKØDÅQTSVTDYQVNQAANLVBCLSDELYPNEKRMLMDAVKEAKRLVQA
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                           RNLLQDTGFNRING--ENGWTGSTGIEVABGDVLFKDRSLRLTSAREIDTETYPTYLYQQ
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             DLTENTFDLATIGTAFFFSNYSDSLTVGADSPASGGEVYVDKFELI PVNATFEAEEDLDV
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A;Cross-references: EMBL:X06711; NID:g40264; PIDN:CAA29898.1; PID:g580949
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.1%; Score 2547.5; DB 2; 43.8%; Pred. No. 1.3e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crystal protein
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PHIDSIRFVETEK 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Start codon: 110
C;Superfamily: parasporal cr
C;Keywords: delta-endotoxin
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A; Molecule type: DNA
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Superfamily: pare
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N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
S;Species: Bacillus thuringiensis
C;Daccession: S39536
R;Shevelev, A.B.; Svarinsky, M.A.; Karasin, A.I.; Kogan, Y.N.; Chestukhina, G.G.; Stepar
FEBS Lett. 336, 79-82, 1993
A;Reference number: S39536; MUD:94085596; PMID:8262221
A;Reference number: S39536
A;Recension: S39536
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SIRS
A;Cross=references: EMBL:X75019
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                            SHWDAQVSQQLRVNPNCKYVLRVTARRVGGGGGYVTIRDGAHHQBTLJFNACDYDVNGTY 1114
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IPGINYEIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQQDGNMHFLVL 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERNYGTITSNKIKYYDLANKDIPQVRS---LGADLANYYAQVYGVPYASFTLLDKNTGSG 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVRA-NLVLQRFBILHALFVSSMPSFG-SGPGSQRFQAQLLVVYAQAANLHLLLLADABK 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFSEVESAVIRSPHLPDILSEIBFYTTRAGLPLNNTEYLBYWVGHSI--KYKNTNASSAL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVGGFTYSKPHTTMQVCTQNYNTIDEIP--PENEPLSRGYSHRLSHITSYSF----SK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYKDYLKMSEGDYIDSYINPGNV--RIGLQTGIDIVAVVGALGGPVGGILIGFLSTLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTRARSVVVTQYIALBLDFVAKIPSPAISGQ-----EVPLLSVYAQAANLHLLLRDASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGAEWGFTPGEISTFYDRQV-TRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLLVLDLVALFPNYDTRTYPIETTAQLTREVYTDPIVPNRETSGGF----CRRWSLNSDI
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                                                                                                    ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEER 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 45.5%; Score 2750.5; DB 2; Local Similarity 48.7%; Pred. No. 1.9e-151; Hes 562; Conservative 197; Mismatches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498
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DPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELWPRGR-DQWEIFLEHVEQ LIDOKITDSVRKTALAGLGGGGLDVYQKSLKWMLENRDDTRARSVVYTQYIALBLDFV [- - - - - - - - - - - - - -	SLGADLANYYAQVYCPYASPTILDEXNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBI	SGGEVYUDKELIPUNATFEAEEDLDVAKKANNGLFTSKKD-ALQTSVTDYQVNQAANLV	ALENNOENG-INSSDENARSPHIDTGEDDINENTGIWVVFKIPTINGYATIGALLEUEEG :
VLGVPPAGQLASFY GDGLDVYQKSLKW	SFTLLDKNTGSGSV RFNFTNPQNISDR- SYSFSKNASSPARY IILQSR FTGGNILKRTSSGP	EEDLDVAKKAVNGI : : EYDLERAQEAVNAL AKELSDERNILODF AKELSDERNILODP KORSILELTSAREID KORSILELTSAREID : IVKNYPDNILPD ETLDVEGTESIMEI	HIDYGEIDLMENTG DIDVGCTD[HENI] ARKRGASEKAYYAA ::::: EKLQLETKRYTEA EKQLETKRYTEA HIS PGVNAEIPEELGH NAMSQUSQUFTVQP :: EWBAEVSQAVRVCP
TVOTGINIAGRILG DSVRKTALAGIGGI ::	- MYYAQVEYPA :	DKFELIPVNATFEA	NG-NMSSDSHAFSE OGEKCAHHSHIPSL DGEKCAHHSHIPSL ERACOCOECOWODKA ERACOCOECOWODKA ERACOCOECOWODKA SENTERAYLSELPVI HAIREAYLSELPVI NVOCLEDTSVLVIP I
43 102 102 181 162 241 222 282 282 361 361	392 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	651 710 710 681 751 741 810	866 856 925 916 976 1045 1105
4 6 8 6 8 6 8 6 8	8 4 8 4 8 4 8 4 8	6 8 6 8 6 8 6	8 4 8 4 8 4 8 4 8

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parasporal crystal protein cry7Aal - Bacillus thuringiensis
NyAlternate names parasporal crystal protein cryIIC
C;Species: Bacillus thuringiensis
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
C;Accession: A48944
R;Lambert, B.; Hofte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M.
Appl. Environ. Microbiol. 58, 2536-2542, 1992
A;Title: Novel Bacillus thuringiensis insecticidal crystal protein with a silent activi
A;Reference number: A48944; MUID:92384571; PMID:1514800
A;Contents: BTS137J
A;Accession: A48944
A;Molecule type: DNA; protein
A;Residues: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-1138 <LAM>
17;
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A;Note: sequence extracted from NCB1 backbone (NCBIN:112092, NCBIP:112093)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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FIVDSVBLLLAMEE 1228
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ce extracted from NCBI backbone (NCBIN:92865, NCBI) parasporal crystal protein	Query Match 36.3%; Score 2191; DB 2; Length 1156; Best Local Similarity 41.5%; Pred. No. 5.7e-119; Matches 501; Conservative 195; Mismatches 414; Indels 98; Gaps 24;	5 NONEYEILDASSSTSVSDNSVRYPLANDQTTTLQNANYKDYLRMSEGENPELFGNPETFI 64 : : : : : : : : : 2 NONKHGIIGASNCGCASDDVAKYPLANNPYSSALNLASC 40	65 SSSTVQTGIGIVGQVKGALGVP-FAGGIASFYSFIVGQLWPSSTVSVWE 112	113 MIMKQVEDLIDQKITDSVRKTALAGLGGLGDGLDVYQKSLKNMLENRNDTRARSVVVTQY 172 	173 IA-LEEDFVAKIPSFAISGQBVPLLSVYAQAANLHLILERDASIPGABWGF 222 	223 TPGEISTFYDRQYTRTAQYSDYCVKWYNTGLDKLKGTNAASMLKYHQFREWTLLVKD 280	281 LVALPPNYDTRTYPIETTAQLERBVYTDPIVFNRRTSGGFCRRWSLNSDISF 332 : :	333 SEVESAVIRSPHLFDILSBIBFYTTRACLPLN-NTEYLEYWVGHSIKYKNTNASSALBRN 391 :: : :	392 YGTITSNKIKYYDLANKDIFQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSG 445 	446 SVGGFTYSKPHTTMQVCTQNYNTIDEIPPENBPLSRGYSHRLSHITSYSFSKNASSPA 503 443 YIRTTGIDNPRVQNINTYLPGENSDIPTPEDYTHILSTTIN.TGGLQVASN 494 504 RYGNLPVPAMTHRSADVTNTVYSDKITQIPTVRAHTLVSGTTVIKGPGFTGGNILKRISS 563 495 RRSLVMTGMTHKSLARNITINPDRITQIPTKVDTRGTGVSVYNDPGFTGGALLQRTDH 554 564 GPLAYTSVSVKSPLSQRYRARIRYASTTMLRLEVTIS-GTRIYSINVNTTWNKGDDLTFN 622 628 RRSLVMTGMTHRSADRITVGADSFASGTGVVVDKFELIPVNATPERAEDLDVAKKAV 682 1
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502 AVKMYKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPLSQKYRVRVRYATNVSG 594 RLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADS 594 RLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADS 595 QFNVYINDKITLQTKPQNTVETIGEGKDLTYGSFGYIEYSTTIQFPDRHPKITLHLSD	OY 649 FASGGBYYDRFELIPWATFEAEBDLDVAKGANNGLFTSKCALQTSYTDYQVNQAANL 708 ::	Qy 709 VECLSDELYPNEKRALWDAVKEAKRLVQARALLQDTGFNRINGENGWTGSTGIEVAEG 766 : : : :: : :: Db 680 VDCISGDELYPNEKRELGNLVKYAKRLSYSRNLLLDPFFDSINSSEENGWYGSNGIVIGNG 739	Qy 767 DVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLIRH 826 :	QY 827 RANQIVKNVPDNILPDVLPVNSCGGIDRCSEQQYVDANIALENNGENGNESDSHAFSFH 886 197 DAKHRILDVSDNILPDILPENRCAAQQYLDENPSPECSSMQDGILSDSHSFSLN 856	OY 887 IDTGEIDLAENTGIWVVFKIPTINGYATLGNLELVEEGPLSGETLERAQQGEQWQDRAA 946	Qy 947 RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006 1	Qy 1007 GRAYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066	Qy 1067 WNSQVSQQFTVQPNYRYVLRYTARKEGVGDGYVIIRDGANQTETLIFNICDDDGVLSAD 1126	Qy 1127 QTSYITKTVEFTPSTEQVWIDMSETEGVPNIESVELVLEEE 1167 :	RESULT 6 S19306 parasporal crystal protein cry9Aal - Bacillus thuringiensis NiAternate names: delta-endotoxin; insecticidal crystal protein; parasporal crystal protein Cipecies: Bacillus thuringiensis Cipate: 04-06-1922 #texquence revision 04-06-1992 #text_change 01-06-2000 Cipate: 04-06-1925 #sequence revision 04-06-1992 #text_change 01-06-2000 R;Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyrc FEBS lett. 293, 25-28, 1991 A;Title: Nucleotide sequence of a novel delta-endotoxin gene cryig of Bacillus thuringic A;Residues: 359306 A;Recession: 359306 A;Rocession: 2036B A;Rocession: 3036B A

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1111 SYTDGRRDNPCESNRGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELL 1170
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C;Species: Bacillus thuringiensis
C;Species: 20-Feb-1995 #text_change 01-Dec-2000
C;Accession: 832645
R;Lambert, B.
R;Lambert, B.
R;Lambert, B.
R;Lambert, B.
R;Reference number: 832645
A;Reference number: 832645
C;Superfamily: parasporal crystal protein
C;Reywords: delta-endotoxin
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                                                                                                                                                YRARIRYASTINLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                753 DLEIYLIRYNAKHETVNVLGTGSLWPLSVQSPIRKCGEPNRCA--PHLEWNPDLDCSCRD
TONYNTIDEIPPENEPLS - - RCYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADV
                                                                 TNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQR
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paragoral crystal protein crylFal - Bacillus thuringiensis (strain aizawai)
paragoral crystal protein crylFal - Bacillus thuringiensis (strain aizawai)
N;Alternate names: parasporal crystal protein crylF
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C;Accession: A44459
R;Chambers, J.A.; Jelen, A.; Gilbert, M.P.; Jany, C.S.; Johnson, T.B.; Gawron-Burke, C.
J. Bacteriol. 173, 3966-13976, 1991
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene from A;Recension: A4459
A;Accession: A4459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1174 <CHA>
A;Cross-references: GB:MG3897; NID:g142757; PIDN:AAA22348.1; PID:g142758
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                                NGLSDWINATSDVINVQQLSDTSVLVIPNWINSQVSQQFTVQPNYRYVLRVTARKEGVGDGYV
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1149 IEFVBTEK 1156
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Query Match 34.6%; Score 2093.5; DB 2; Length 1166; Best Local Similarity 39.7%; Pred. No. 2.7e-113; Matches 482; Conservative 172; Mismatches 392; Indels 167; Gaps 24;	59 NPETFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLMPSSTVSVW 111	112 EMINKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQ 171 ::::	172 YIALELDFVAKIPSFAISGGEVPLLSVYAQAANLHLLLLRDASIFGAEMGFTPGEISTFY 231 132 PRLTDDAIVTGLPTLAIRNLEVVNLSVYTQAANLHLSLLRDAVYFGERWGLTQANIEDLY 191	232 DRQVIRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREWTLLVLDLVALPPNYDTR 291 : : -	292 TYPIBTTAQLTREVYTDPIVFNRETSGECRRWSLASDISFSEVBSAVIRSPHLFDILSE 351	352 IEFYTTRAGLPLANTEYLEYWVGHSIKYKOTNASSALERNYGT394 	395 ITSNKIKYYDLANKDIPQVRSLGADLANYYAQVYGVPYASFTILLDKNTGSGSVGGFT-YS 453 	454 KPHTIMQVCTQNYNTIDEIPPENBPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVF 511	512 AWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRISSGPLAYTSV 571 	572 SVKSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMRKGDDLTFNTFDLATIGT 631 :::	632 AFTFSNYSDSLTVGADSPASGGEVYVDKFELIPVNATFRAREDLDVAKKAVNGLFTSKKD 691 : : :	692 -ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLMDAVKBAKRLVQARNLLQDTGFNRIN 750 :	751GENGWTGSTGIEVARGDVLFKDRSLRLISAREIDTETYPTYLYQQIDBSLLKPYTRYK 808 	809 LKGFIGSSQDLEIKLIRHRANQIVRAVPDNLLPDVLPVNSCGGIDRCSBQQYVDAN 864	865 LALENNGENG-NMSSDSHAFSPHIDTGEIDLARBYGIWVPKIPTTNGYATLGNLELVEB 923 	GPLSGFTLERAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	854 KPLIGEALARVKRAEKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAM 913 984 MLAAQNIVQSIPYVYNDALPEIPGANYTSFTELTNRLQQAWNLYDLRNAIPNGDPRNGLS 1043	
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                       500 SSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILK 559
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references: GB:M16463; NID:g143098; PIDN:AAA22551.1; PID:g143099
amily: parasporal crystal protein
ds: delta-endotoxin
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1154 FIVESVELLLMEE 1166
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A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: BMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
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R;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerc
A;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe, C.; Vandekerc
A;Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thu
A;Reference number: A26461; MUD:87054026; PMID:3023091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residuse: 1-730,'L',732-784,'R',786-1155 <HOP>
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1-15.
C;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 IWGIFGPSQ----WDAFLVQIEQLINQRIEBEPARNQAISRLEGISNLYQIYAESFREWEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 NPBL------FGNPBT-FISSSTVQTG---IGI---VGQVLGALGVPFAGQIASPYSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLYQPLLSBEVPGAGFVLGLVDI
                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-1155 < WAB>
A; Cross-references: GB:M13898; NID:g142719; FIDN:AAA22330.1; PID:g142720
A; Cross-references: GB:M13898; NID:g142719; FIDN:AAA22330.1; PID:g142720
A; Experimental source: subsp. berliner
B; Chak, K.F.; Jen, J.C.
submitted to the BMBL Data Library, October 1990
A; Description: Complete nucleotide sequence and expression in Escherichia A; Reference number: S14555
A; Accession: S14555
A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124
A;Experimental source: subsp. kurstaki
R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A.
                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.1%; Score 2061.5; DB 2; Length 1155; Best Local Similarity 39.3%; Pred. No. 1.9e-111; Matches 478; Conservative 185; Mismatches 387; Indels 167;
                                                                                      DNA 5, 305-314, 1986

A;Title: Bacillus thuringiensis entomocidal protoxin gene sequence A;Reference number: A90955; MUID:86300092; PMID:3743328

A;Accession: A90955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cromment: This toxin is lethal to the larvae or Lepicote Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: parasporal crystal protein
C;Reywords: delta-endotoxin
F;82-586/Product: toxic peptide #status predicted
F;82-386/Region: toxic #status predicted
F;300-586/Region: insecticidal #status predicted
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parasporal crystal protein crylAb3 - Bacillus thuringiensis
NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal procises: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 01-Dec-2000
C;Accession: A90025; A91560; A90955; S14555; A26461; A2472; A29043; JD0002
R;Kondo, S.; Tamura, N.; Kunitate, A.; Hattori, M.; Akashi, A.; Ohmori, I.
Agric. Biol. Chem. 51, 455-463, 1987
A;Ritle: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from A;Reference number: A90025
A;Accession: A90025
A;Accession: A90025
A;Accession: Boource: subsp. kurstaki
A;Reserimental source: subsp. kurstaki
C;Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
A;Reference number: A91560; MUID:8716305; PMID:3557124
A;Residues: 1-1155 cGEI>
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                                                                                                             620 TFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVDKFELIPVNATFEAEEDLDVAK
                                                                                                                                                                                                                                  S62 OSGSFRTVGFTTPFNFSNGSSVPTLSAHVPNSGNEVYIDRIEFVPAEVTFRAEYDLERAO
                                                                                                                                                                                                                                                                                                                                                             VSIIR----APMFSWIHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGPTGGDILR
                                                                            RTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDL
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1136 IGETEGTPIVDSVELLEMER 1155
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                                                                                                                                                                                                                                                                                                                S-IRSPHLMDILNSITIYT----DAHRGEY--YWSGHQIMASPVGFSGPBFTFPL---Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ABWGFTPGBISTPYDROVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLDLVALPPNYDTRTYPI BITTAQLTREVYTDPIVPNRETSGGPCRRWSLANSDISFSEVES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 VGGPTYSKPHTTMQVCTQNYNTIDBIPPENE--PLSRGYSHRLSHITSY--SPSKNASSP
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                                                                                                                                                                                                                                                                       158 NRNDTRARSVVVTQYIALELDPVAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIMGNAAPQQRIVAQLGQGVYRTLSSTL---YRRPFNIGINNQQLSVLDGTEFAYGTSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 ARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILKRTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDTGPNRING---ENGWTGSTGIEVAEGDVLFYDRSLRLTSAREIDTETYPTYLYQQIDES
                                                                                                                                                                                       34.0%; Score 2052.5; DB 2; Length 1155; 39.4%; Pred. No. 6.3e-111;
J. Mol. Biol. 208, 183-194, 1989
A; Title: Functional mapping of an entomocidal delta-endotoxin. 8
A; Ritle: Functional mapping of an entomocidal delta-endotoxin. 8
A; Recession. 804994; MUID:89362455; PMID:2769751
A; Rocession. 804994; MUID:89362455; PMID:2769751
A; Rocession. 804994; A, 451-724 «HAM»
A; Residues: 429-449; A', 451-724 «HAM»
A; Experimental source: strain aizawai IC1
C; Comment: This toxin is lethal to the larvae of lepidopterans of; Ropywords: delta-endotoxin
C; Keywords: delta-endotoxin
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N;Alternate names: delta-endotoxin ICl; entomocidal crystal protein
C;Species: Bacillus thuringiensis
A;Variety: strain aizawai ICl
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 01-Dec-2000
C;Accession: S02134; S04994
R;Haider, M.Z.; Ellar, D.J.
R;Haider, M.Z.; Ellar, D.J.
Nucleic Acids Res. 16, 10927, 1988
A;Title: Nucleotide sequence of a Bacillus thuringiensis aizawai ICl entomocidal cry
A;Accession: S02134
A;Accession: S02134; MUD:89083518; PMID:3205732
A;Accession: S02134
A;Status: translation not shown
A;Molecule type: DNA
A;Ctose-references: EMB:X13233; NID:940277; PIDN:CAA31620.1; PID:940278
A;Experimental source: Strain aizawai ICl
R;Haider, M.Z.; Ellar, D.J.
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                     ARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILKRTS
                                  SGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLPVTISGTRIYSINVNKTMNKGDDLTPN
                                                                                                                                             TPDLATIGTAPTFSNYSDSLTVGADSFASGGBVYVDKPBLIPVNATFBAEEDLDVAKKAV
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C;Species: Bacillus thuringiensis
C;Species: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C;Accession: JC2219
R;Udayssuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
B;Udayssuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
A;Udayssuriyan, V.; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
A;Title: Cloning of a new crylA(a) gene from Bacillus thuringiensis strain EA;Reference number: JC2219; MJID:94289859; PMID:7764972
                                                                                                                                                                                                                                                                                                                                                                                                          PS-----TIYRORGTV------DSLDVIPPQDNSVPPRAGPSHRLSHVTMLSQAAGAV
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                                                                                                                                                                YTLR---APTPSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRR
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JT0241
paragoral crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
N;Alternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
C;Accession: JT0241
R;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
A;Shimizu, M.; Oshie, K.; I565-1573, 1988
A;Title: Cloning and expression in Bscherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Molecule type: DNA
A;Residues: 1-1176 <SHI>A;Molecule type: DNA
A;Rosidues: 1-1176 <SHI>A;Note: b thuringiensis aizawai IPL7 produces similar 130K and 135K insecticidal protein
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larva
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                VLDIVALPSNYDSRRYPIRTVSQLTREIYTNPVLENPDGSFRGMAQRIEQN-----
              -----GKCAHHSHHPSLDIDVGCTDLNBDLGVWVIPKIKTYQDGHARLGNLE
                                            LVEEGPLSGETLERAQQOEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
                                                                                                       EMSDMLAAQNIJVQSI PYVYNDALPBI PGMNYTSPTELTNRLQQAWNLYDLRNAI PNGDPR
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A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Cross-references: DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g535781
C;Genetics: A;Gene: crytA(a)
A;Gene: crytA(a)
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                  53 NPEL-----PGNPET-FISSSTVQTG---IGI---VGQVLGALGVPPAGQIASFYSF
                                                                                                                                              NYGTITSNKIKYYDLANKDIPQVRS-----LGADLANYYAQVYGVPYASPTLLDKNT
                                                                                          Query Match 33.8%; Score 2045; DB 2; Length 1176; Best Local Similarity 39.3%; Pred. No. 1.8e-110; Matches 479; Conservative 174; Mismatches 415; Indels 152;
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parasporal crystal protein cryAel - Bacillus thuringiensis (strain alesti)
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 01-Dec-2000
C;Accession: A41052
R;Lee C.S.; Aronson, A.I.
A; D Bacteriol. 173, 6632-6638, 1991
A;Title: Cloning and analysis of delta-endotoxin genes from Bacillus thuringiensis subs. A;Reference number: A41052; MUID:92011442; PMID:1655719
A;Accession: A41052
A;Status: preliminary
A;Molecule type: DNA I PNGDFRNGLSDWNATSDVNV-QQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLRVTARK 1091 : : || .| | .| || : || | : || | : || : || : || : || : || : || : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : || : : | 392 : |||||||||: | || || || S-IRSPHLMDILNSITIYTDAHG-----GYYYWSGHQIMASPVGFSGPEFTFPL---Y 338 446 63 IVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLE 158 NRNDTRARSVVVTQYIALELDFVAXIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFG | | | : | | : | | : | | : | BGYGEGCVTIHEIENNTDELKESNCVEERIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYN 1119 DTGVLSADQTS-----YITKTVEFTPSTEQVWID 53 NPEL------PGNPET-PISSSTVQTG---IGI---VGQVLGALGVPRAGQIASFYSF AVIRSPHLFDILSBIBFYTTRAGLPLNNTBYLEYWVGHSIK-----YKNTNASSALBRNY GTITSNKIKYYDLANKDIPQVRSLGADLANYYAQ--VYGVPYASPTLLDKNT----GSGS OKLINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMYTSFTELTNRLQQAWNLYDLRNA 4 NPKINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLIQFLLSBFVFGAGFVLGLIDL Query Match 33.8%; Score 2044.5; DB 2; Length 1181; Best Local Similarity 39.0%; Pred. No. 1.9e-110; Matches 477; Conservative 190; Mismatches 404; Indels 151; Gaps A;Residues: 1-1181 <LEB>
A;Residues: 1-1181 <LEB>
A;Crose-references: GB:MS522; NID:g142874; PIDN:AAA22410.1; PID:g142875
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin Length 1181; EGVGDGYVIIRDGANQTETLTFN------ICDD-----: |||| | ::||||:| || 1157 IGETEGTPIVDSVELLLAMER 1176 MSETEGVFNIESVELVLEER 1167 1037 1033 1092 1097 1148 98 120 338 290 393

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VEMSDMIAAQNIVQSIPYVYNDALPEIPGAAYTSFTELTURLQQAWNLYDLRNAIPNGDF 1038
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                                                                                        Indels 168;
                                                     Length 1156;
                                                   Query Match
33.8%; Score 2043; DB 2;
Best Local Similarity 39.1%; Pred. No. 2.2e-110;
Matches 476; Conservative 185; Mismatches 389;
C;Superfamily: parasporal crystal protein C;Keywords: delta-endotoxin
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C; Accession: A29125
B; F; Fischhoff, D.A.; Bowdish, K.S.; Perlak, P.J.; Marrone, P.G.; McCormick, S.M.; I Bio/Technology S; 807-m13, 1987
A; Title: Insect tolerant transgenic tomato plants.
A; Reference number: A29125
A; Accession: A29125
A; Status: not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-1156 < FIS>
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ALIGNMENTS

10 A A	RESULT I C8AA BACUK STANDARD; PRT; 1157 AA.
2 E E	2001 (Rel.
125	(Rel. 40,
08 08	(Crystaline entomocidal protoxin) (
e e	protein). CRYSAA OR CRYVIIIA(A).
SS	Bacillus thuringiensis (subsp. kumamotoensis).
38	Bacteria; rimicutes; baciliales; baciliaceae; bacilius. NCBI TaxID=132267;
RN :	
8 G	SEQUENCE FROM N.A. STRAIN-NRR. R-18746 / DSSOC:
æ	Payne J.M., Sick A.J., Foncerrada L.;
RT	"Novel coleopteran-active Bacillus thuringiensis isolate and a novel
X 0	gene encoding a coleopteran-active toxin."; Datent number RDN498537 12-AM3-1992
ខ្លួ	-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
ပ္ပ	EPITHELIAL CELLS OF COLEOPTERA.
ប្ជ	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
ខ្ល	sportlation and is accumulated both as an inclusion and as part of
38	The spore coat.
ខ	
႘	-!- SIMILARITY: Belongs to the delta endotoxin family.
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ဗ င	This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
9 8	the Buronean Bioinformatics Institute. There are no restrictions on i
ខ្លួ	use by non-profit institutions as long as its content is in no w
ပ္ပ	modified and this statement is not removed. Usage by and for commerci
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ပ္ပင္ပ	or send an email to licensewisd-sib.cnj.
3 8	EMBL: U04364: AAA21117.1:
g	HSSP; P07130; 1DLC.
8	IPR001178;
<u>8</u>	InterPro; IPR005638; endotoxin C.
ž 2	InterPro; IPROUS639; enactoxin N. InterPro: IPROU8979: Gal bind like.
ž	
8	Pfam; PP03944; endotoxin_C; 1.
žž	Fram; Frosts; Encountries; 1.
8	SEQUENCE 1157 AA; 131009 MW; 687B5C49DE93683B CRC64;
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Agron R. Takeuchi F. Golwara K., Minami M., Kaji Y., Suzuki N., Andrin H., Asano S., Obba M., Iwahana H.;
Hori H., Asano S., Obba M., Iwahana H.;
Toloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringiansis serovar japonensis strain buibui toxic to scarabaeid insects.";

Lurr. Microbiol. 28:15-19(1994).

By EBQUENCE OF 1-14 AND 56-64, AND CHARACTERIZATION.

PREDITES-955559; Pubbed-as-200856;
MINIMES-955559; Pubbed-as-200856;
Minami M., Asano S., Sator R., Obba M., Iwahana H.;
Hori H., Suzuki N., Ogiwara K., Himmjima M., Indrasith L.S.,
Minami M., Asano S., Sator R., Obba M., Iwahana H.;
Tolaracterization of larvicidal toxin protein from Bacillus
thuringiensis serovar japonensis strain Buibui specific for scarabaeid beetles.";
J. Appl. Bacteriol. 76:307-313(1994).

L. FUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS. ACTIVE ON VARIOUS SCARABAEID BERILES
C. SUCH AS ANDMALA CUPREA, A. RUPCOUPREA AND POPLICAL JANCHALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry8Ca (Insecticidal delta-endotoxin CryVIIC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis (subsp. japonensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TaxID=128936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminus.
SIMILARITY: Belongs to the delta endotoxin family.
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llarity 64.2%; Pred. No. 4.4e-205;
Conservative 109; Mismatches 257;
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PSTEQVWIDMSBTEGVFNIBSVELVLEER
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InterPro; IPR00879; Gal_bind_like.
Pfam; PP00555; endotoxin_1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
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MEDLINE=94100786; PubMed=7764305;
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InterPro; IPR005638; endotoxin_C.
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                                                                                                                                                                                                                                  STANDARD;
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HSSP; P07130; 1DLC.
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SEQUENCE 1160 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
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1139
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045706;
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QQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLRVTARKBGVGDGYVI I RDGANQTBTLTP
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InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
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                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                CRYBBA OR CRYVIIIB(A)
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=132267;
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SEQUENCE PROM N.A.
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Q45705;
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ELTREIPTDPV-----GSYVTQQSSTLISWYDMIPAALPSFSTLEN-LLRKPDFPTLL 352
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                                                                               ETPISS-STVOTGIGIVGOVICALGVPFAGQIASPYSPIVGQLMPSSTVSVWEMIMKQVB 119
                                                                                                                                             DLIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
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                   VAKIPSFAISGOEVPLLSVYAQAANI.HILLIRDASIFGAEWGFTPGEISTFYDRQVTRTA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Patent number W09315206, 05-AUG-1993.
-- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-- EPITHELIAL CELLS OF INSCTS. ACTIVE ON WARIOUS SCARABARID BEFILES.
-- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MSPNNQNBYELLDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
1047 QQLSDISVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKBGVGGGYVIIRDGANQTBTLIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the spore coat. -- MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michaels T.E., Foncerrada L., Narva K.E.; "Process for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pesticidial crystal protein crysBa (Insecticidal delta-endotoxin
cryvIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
                                                                                        84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1169;
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52.2%; Score 3152; DB 1; Length 1
Best Local Similarity 54.0%; Pred. No. 6.4e-172;
Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00555; endotoxin; 1.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
Toxin; Sporulation.
SEQUENCE 1169 AA; 133543 MW; 22EEPCF5ED699909 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                           QLIRBVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIBFYTTRA 359
                                                                                                                                                                                                                                               360 GLPLANTEYLEYWCHSIKYKNTNASSALERNYGT-----ITSNKIKYYDLANKDIPQVR 414
                                                                                                                                                                                                                                                                                  S--FTSDRYMRYWAGHQISYKHIGTSSTFTQMYGTNQNLQSTSN----PDFTNYDIYKTL 410
                                                                                                                                                                                                                                                                                                                                        | | | | : : : : : : : : : SNGAVLLDIVYPGYTYTPFGMPETEPMVNQLANTRKT--LTY-KP-ASKDIIDRTRDSE 466
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BLINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSRALRDVRNRFBILDSLF 180
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                                                                                                                         AS -- TINLRLP-VIISGTRIYSINVNKT-MNKGD-DLTFNTFDLATIGTAFTFSNYSDSL
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                                   VAKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
                                                     QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYP1ETTA
                                                                                                                                                                                                                                                                                                                    SLGADLAN----YYAQVYGVPYASPTILIDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTI
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ESVELIVDVE 1169
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

STRAIN-BIF502618A;
MEDLINE-96141404; PubMed-8572715;
MAIN-BIF502618A;
MAIN-BIFF502618A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the terminus.
                                                                                                                             CryixC(a)) (Crystaline entomocidal protoxin), (130 kDa crystal protein). (20 kDa crystal protein). (20 kDa crystal protoxin). (20 kDa crystal protoxin).
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SEQUENCE 1157 AA; 129775 NW; C364391EF7FDFBBA CRC64;
                                                                                                                                                                                                                                                Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Firmicutes; Bacillales; Bacillacese; Bacillus.
NCBI_TaxID=1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the delta endotoxin family.
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Matches 619; Conservative 195; Mismatches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.7%; Score 3123; DB 1; 52.3%; Pred. No. 2.8e-170;
                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
6-CCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ca (Insecticia
1157 AA
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PRR, A59350; S4247.
HSSP, P07130; 1DLC.
INTERPRO; IPR001178; Endotoxin.
INTERPRO; IPR005639; endotoxin.
INTERPRO; IPR008639; endotoxin. N.
INTERPRO; IPR008679; Gal_bind_like.
Pfam; PP03944; endotoxin_l.
Pfam; PP03945; endotoxin_l.
   C9CA BACTO
045733;
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                                                                                                                                                EGDVLFKDRSLRLTSAREIDTETYPTVLYQQIDESLLKPYTRYKLKGFIGSSQDLRIKLI 824
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QLTREVYTDPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLPDILSEIEPYTTRA
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                                                                  VAKI PSPAISGQEVPLLSVYAQAANLHLLLLRDASI PGAEWGPTPGBISTPYDRQVTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSPNNQNEYELLDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGE----NP
                                                                                                                                                                                                                                                                                                                                                                                     Midoh N., Oyama K.;
"Bacillus thuringiensis cry gene for insecticidal crystal protein.";
Submitted (PEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BPITHELIAL CELLS OF INSECTS.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the spore coat. MISCELLANBOUS: Toxic segment of the protein is located in the
                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry9Ea (Insecticidal delta-endotoxin CryIXE(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;
                                                                                                                                                                                                                                                           Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.7%; Score 2825.5; DB 1;
llarity 48.6%; Pred. No. 2.6e-153;
Conservative 197; Mismatches 364;
                                                                                                                                                                                                            Bacteria, Firmicutes; (subsp. aizawai).
NCBI_TaxID=1433;
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1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P07130; IDLC.
InterPro; IRR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
InterPro; IRR008639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PP00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB011496; BAA34908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP03944; endotoxin_N; 1. Pfam; PP03945; endotoxin_N; 1.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin; Sporulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 574; Conserv
                                                                                                                                                                                                                                                                                                                    [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SSK-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           terminus
  BACTA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNNDIYQIISQVSNFASPVGSSYSVWDTNFYL----SSGQVSGISGYTQQGIPAVCLQQ 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLIDOKITDSVRKTALAGLOGIGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSNLQILVNYQTNGSA-------WRGSRVRYHYLHSSIIQBKSYGLLSDPVGANINV 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNTIDEIP---PENBEDLSRGYSHRLSHITSYSFSKANS-SPARY-GNLPVFAWTHRSADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTPIS-SSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVWEMINKQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANKOI FQVRSLGADLANYYAQVYGVPYASFTLLDNATGSGSVGGPTYSKPHTTMQVCTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 VAKIPSPAISG-----QEVPLLSVYAQAANLHLLLIRDASIPGAEWGPTPGEISTFYDRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 IETTAQLTREVYTDPIVFN--RETSGGFCRRWSLN----SDISFSEVESAVIRSPHLFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSBIEP---YTTRAGLPLANYTEYLEYWYGHSIKYKNTNASSALERNYGTITSNKIKYYDL
                                                                                                  nitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BRITHELIAL CELLS OF INSECTION.
BRITHELIAL CELLS OF INSECTION.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                 the spore coat. 
MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; Sporulation. _ SEQUENCE 1169 AA; 132228 MW; 659AB257229DB5E9 CRC64;
                                                                                                                                                                                                                                                            terminus.
SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%; Score 2715; DB 1; larity 46.9%; Pred. No. 5.3e-147; Conservative 204; Mismatches 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001178; Endocoxin.
InterPro; IPR005638; endocoxin.
InterPro; IPR005639; endocoxin.N.
InterPro; IPR006979; Gal.bind_like.
Pfam; PP00555; endocoxin, 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endocoxin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D85560; BAA19948.1; -.
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    NCBI_TaxID=128936;
                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               558;
                                                                                         ABano S.;
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GDVLFKDRSLRLTSARBIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLKIKLIR 825
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                                                                                                                                                   FOVRSLGADLANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTID
                                                                                                                                                                              RAIDSRARNFGNLYANLYGV--SSLNIPP--TG-----VMSEITNAANTCRQDLTTTE
                                                                                                                                                                                                                                                                                                                                              GGPFFKGRALQLASAR----ENYPTYIYQKVDASTLKPYTRYKLDGFVQSSQDLEIDLIH
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry9Da (Insecticidal delta-endotoxin CryIXD(a)) (Crystaline entomocidal protoxin) (132 kDa crystal
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CRY9DA OR CRYIXD(A).
Bacillus thuringiensis (subsp. japonensis).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                            VYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQL 1056
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                                                                                                                                                                                                                                                                                                   SSDSHAPSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQ 936
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30-MAY-2000 (Rel. 39, Last sequence update)
16-GCT-2000 (Rel. 40, Last annotation update)
16-GCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylka (Insecticidal delta-endotoxin
CrylKa)) (Crystaline entomocidal protoxin) (137 kDa crystal protein)
CRYLKA OR CRYLK(A) OR CRYLK.
Bacillus thuringlensis (Subsp. morrisoni).
Bacillus pirmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                              YRARIRYASTTNLRLPVTISGTRIYSINVNKTMNKGDDLTPNTFDLATIGTAFTFSNYSD
                                                                                                               SLTVGADSPASGGEVYVDKFELI PVNATFEABEDLDVAKKAV-NGLFTSKXDALQTSVTD
                                                                                                                                                                                                         STGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQ
 RNSTDELPSLNPEGD-IIRNYSHRLSHITQYRFQATQSGSPSTVSANLPTCVWTHRDVDL
                        TNTVYSDKITQI PVVKAHTLVSGTTVI KGPGPTGGNI LKRTSSGPLAYTSVSVKSPLSQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=190;
MEDLINE=56,102856; PubMed=8586263;
MEDLINE=56,102856; PubMed=8586263;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
Koo B.T., Park S.-H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
Factoning of a novel crystal protein gene crylk from Bacillus
thuringiensis subsp. morrison!";
PENS Microbiol. Left. 134:159-164(1995).
-!- FUNCTION: PROMOTES COLLODGSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEIA RAPAE
AND NOT ACTIVE ON PLUTELLA XYLOSTELLA.
-!- DEVELOPMENTAL STARE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYDVNGTYVNDNSYITBEVVFYPETKHMWVBVSESEGSFYIDSIEFIETQE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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  MISCELLANEOUS: Toxic segment of the protein is located
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                                      SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.9%; Score 2714; DB 1;
llarity 46.3%; Pred. No. 6.4e-147;
Conservative 194; Mismatches 351;
                                                                                                                                                                                                                                                                        InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind Ilke.
Pfam; Pr00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1215 AA; 137378 MW;
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF03944; endotoxin_C; 1. Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                   EMBL; U28801; AAB00376.1; -. HSSP; P02965; ICIY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 581; Conserv
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InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                               1229 AA; 139769 MW;
                                                                                                                                                                                                                                                                       Pfam; PF00555; endotoxin; 1.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
                                                                                                                     EMBL; L32020; AAA22344.1;
HSSP; P02965; 1CIY.
                                                                                                                                                                                                                                                                                                                                                          Toxin, Sporulation
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EVYVDKPELIPVNATPEAEEDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQAANLVECL
                             SDELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRING--ENGWTGSTGIEVAEGDVLF
                                                                                                                               SDEFCLDKKRELLEBYKYAKRLSDERNLLQDPTFTSISGQTDRGWIGSTGISIQGGDDIF
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
80-MAY-2000 (Rel. 39, Last annotation update)
81-MAY-2000 (Rel. 39, Last annotation update)
81-MAY-2000 (Rel. 39, Last annotation update)
8-Seticidial crystal protein crylBb (Insecticidal delta-endotoxin
8-CRYIBB OR (CRYETS)
8-CRYETS
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STRAIN-NRRL B-21110 / EG5847;

DONOVAN W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

DONOVAN W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

DONOVAN W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

DONOVAN W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;

Pacillus thuringinesis cryett and cryet5 toxin genes and proteins toxic to lepidopteran insects.";

Patent number US:322687, 21-JUN-1994.

-! PROCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITELIAL CELLS OF WANY LEPIDOPTERAN LARVAE.

-! DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of the stage of the stage
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MISCELLANEOUS: Toxic segment of the
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Dsage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                Query Match

42.2%; Score 2552; DB 1;
Best Local Similarity 43.2%; Pred. No. 1.1e-137;
Matches 548; Conservative 205; Mismatches 375;
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-ENGWTGSTGIEVAEGDVLFKDRSLRLTSARBIDTETYPTYLYQQIDBSLLKPYTRYKLK 810
                                                                                                                                                                                                                                                                               FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                          GFIGSSODLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLA
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kDa crystal protein)
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MEDLINE=88203216; PubMed=3362680;
Brizzard B.L., Whiteley H.R.;
Nucleotide sequence of an additional crystal protein gene cloned
from Bacillus thuringiensis subsp. thuringlensis.";
Nucleic Acids Res. 16:2723-2723(1988).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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01-NOV-1986 (Rel. 09, Created)
01-NOY-2086 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylba (Insecticidal
CrylBA (S) (Crystaline encomocidal protoxin) (140 |
CRYLBA OR CRYLB(A) OR CRYA4.
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Soetaert P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.1%; Score 2547.5; DB 1; Length 1228; Best Local Similarity 43.8%; Pred. No. 2e-137; Matches 558; Conservative 183; Mismatches 381; Indels 151;
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                                                                                                                                                        EMBL; X06711; CAA29898.1; -.
EMBL; X95704; CAA65003.1; -.
ELR; S00873; S00873.
HSSP; PO7130; 1DLC.
INCEPPO; IPR001178; Endotoxin.
INCEPPO; IPR005638; endotoxin.C.
INCEPPO; IPR009879; Gal bind like.
Pfam; PP00555; endotoxin.1.
Pfam; PP00345; endotoxin.1.
Pfam; PP00345; endotoxin.7.
TOXIN; Sportlation.
                                                                                                                                                                                                                                                                                                                                                                                                                         1228 AA; 139647 MW;
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SIMILARITY: Belongs to the delta endotoxin family

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Toxin; Sporulation
SEQUENCE 1233 AA
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                                                                                               KGPIGSSODLRIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANL 865
                                                                                                                                                                            PLSGETLERAQQOEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLASGVEMSDM 984
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last amotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin
CrylB(c)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYLBC OR CRYLB(C) OR CRYLBC.
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                                                                                                                                              GNGEVYIDKI BI I PVTAT PEARYDLERAQBAVNALFTNTNPRRLKTDVTDYHIDQVSNLV
                                                                   LAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSD
                                                                                                                                                                                                                                                        WINATSDVINVOOLSDISVLVI PHWNSQVSQQFTVQPNYRYVLRVTARKGGVGDGYVIIRDG
                             -GENGWIGSTGIEVAEGDVLPKDRSLRLTSARBIDTETYPTYLYQQIDESLLKPYTRYKL
                                                                                                                                     ALENNGENG-NMSSDSHAPSFHIDTGBIDLNENTGIWVVPKIPTTNGYATLGNLELVBEG
                                                                                                                                                                                                                                                                                                                1096 ENNTDELKFKNREREEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bishop A.H., Bone E.J., Ellar D.J.;
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NVV-1994) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
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DEVELOPMENTAL STAGE: The crystal protein is produced dur sporulation and is accumulated both as an inclusion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis (subsp. morrisoni).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1441;
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                   ECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN-
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1216 PIVDSVELLLMER 1228
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

41.2%; Score 2491; DB 1;
Best Local Similarity 42.1%; Pred. No. 3.4e-134;
Matches 536; Conservative 208; Mismatches 384;
                                                                                                                                                                     InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR008979; endotoxin_N.
InterPro; IPR008979; endotoxin_N.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                           Z46442; CAAB6568.1;
P02965; 1CIY.
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1227 AA;
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                                                                                                                                                                                                                                                                                                                                                                                      NATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGA 1105
                                                                                                                                                                                                                                                                            985
                                                                                                                                    861
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=NRRL B-18872 / PS158C2;
STRAIN=NRRL B-18872 D.A., Cannon R.J.C., Narva K.E., Stelman S.;
Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
Patent number US5723758, 03-MAR-1996
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-BETTHELIAL CELLS OF MANY LEPIDOPTERAN LARVAB.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of the spore coat.
-!- MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 986 AAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBe (Insecticidal delta-endotoxin
CrylB(e)) (Crystaline entomocidal protoxin) (119 kDa crystal protein)
CRY1BE OR CRYIB(E) OR 158C2B.
  -ENGWTGSTGIBVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLK
                          |:|| || : ||: ||: :||: :||: :|| || ||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
                                                                                       GPIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSBOQ----YVDANLA
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SIMILARITY: Belongs to the delta endotoxin family.
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1222 IVDSVELLIMBE 1233
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                                                                                                                                                                                                                                                                                                                            1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                      Indels 134;
                                                                                                                                                                                                                                               Length 1227;
                                                                                                                                                                                                       CBA847BEA0B34CD3 CRC64;
                                                                                                                                                                                                                                           40.7%; Score 2462; DB 1; Local Similarity 42.9%; Pred. No. 1.5e-132; es 542; Conservative 196; Mismatches 392;
                                                           InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; gal bind_like.
Pfam; PP00555; endotoxin_1 1.
Pfam; PP03945; endotoxin_N; I.
Pfam; PP03945; endotoxin_N; I.
Toxin; Sporulation; Plasmid.
                                                                                                                                                                                                         139084 MW;
AF077326; AAC32850.1;
P07130; 1DLC.
                                          InterPro; IPR001178;
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                                                                                                                          LVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATS 1049
                                                                                                                                                                    1050 DVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTE 1109
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                                                   CRDGEKCAHHSHIPSLDI DVGCI DLHENLGVWVVFKI KTQEGHARLGNLRPI BEKPLLGE
                                                                                           SSQDLEIKLIRHRANQIVKNVP -- DNLLPDVL -- PVNSCGGIDRCSEQQYVDANLALENN
           806 DSQDLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCA--PHFEWNPDLDCS
                                                                                 930 TLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGVEMSDMLAAQN
                                                                                                                                                                                                             -----ADQTS-----
                                                                                                                                                                                                                                 1104 ELKFKNCEEBEVYPTDTGTCNDYTAHQGTAACNSRNAGYEDAYEVDTTASVNYKPTYBEE
                                                                                                                                                                                                                                                      -----YITKTVEFTPSTEQVWIDMSETEGVFNIESVELV
                                        GENG-NMSSDSHAPSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the spore coat. MISCELLANEOUS: Toxic segment of the protein is located in the N-
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
80-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry7Aa (Insecticidal delta-endotoxin CryVIIA(a)) (Crystaline entomocidal protoxin) (129 KDa crystal protein).
CRY7AA OR CRYVIIA(A) OR CRYIIIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPPE 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ETPISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVED
                                                                                                                                                                                                                                                                                                                                                                                         476 NEPLSRGYSHRLSHITSYSPSKNASSPARYGN--LPVFAWTHRSADVTNTVYSDKITQIP
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                                                                                                                                                                                                                                                                     Gapa
                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                   Length 1138;
                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                      1138 AA; 129391 MW; 69D8676D4F6A1FAC CRC64;
                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                   40.7%; Score 2458.5; DB 1;
ilarity 43.5%; Pred. No. 2.2e-132;
Conservative 208; Mismatches 400;
                                                        InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; endotoxin N.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
Toxin; Sporulation.
EMBL; M64478; AAA22351.1; --
EMBL; A07236; CAA00646.1; --
PIR; A48944; A48944.
HSCP; P07130; LDLC.
InterPro; IPR001178; Endotox
                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                       514;
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                                                                                                                                                                                      Toxin; Sp
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                                                                                                                                    GMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066
                                                                                                                                                                         WASQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSAD 1126
                                                                                                                                                                                     RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006
         IDTGEIDLMENTGIWVVPKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKMA 946
                                                                                                                                                                                                                                                                                                                                                                                                                                           Payme J.M., Fu J.M.;
Payme J.M.,
Payme J.M.,
"Coleopteran-active toxins.";
Patent number 185286486, 15-FEB-1994.
-!- FUNCTION: PROXOTES COLLODOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA.
-!- DEVELOPMENTAL STACE: The crystal protein is produced during aporulation and is accumulated both as an inclusion and as part of
                                                                                                                                             the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis (subsp. dakota).
Bacteria, Pirmicutes, Bacillales, Bacillus
                                                                                                                                                                                                                   QTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                              PRT; 1138 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR008659; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04367; AAA21120.1; -.
                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 protein).
CRY7AB OR CRYVIIA(B)
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=132268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKAPSHBIQPDLFYWCVHKVSFKKSBQSNLYTTGIYGKTSGYISSGAYSFRGNDIYRTLA 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIREVYIDPIVENREISGGFCRRWSLNSDI--SFSEVESAVIRSPHLFDILSEIEFYITR 358
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                                                                                                                                                                                       |-----DSNRTLANNSLNYPTQXALSPSLKNMYXQDFLSITEREQPEALASG
                                                                                                                                                              1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                      RTPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLWPSSTVSVWBMIMKQVED
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                                                                                                                Gape
                                                                                                                75;
                                                                    Length 1138;
                                                                                                                Indels
                     01DF7072C074CB88
                                                               / Match 40.7%; Score 2458.5; DB 1; Local Similarity 43.1%; Pred. No. 2.2e-132; Les 512; Conservative 218; Mismatches 384;
                     129778 MW;
Toxin; Sporulation.
SEQUENCE 1138 AA;
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                                                  969 MSWLSVVPGVNHPIPTELSGRVQRAPQLYDVRNVVRNGRFLNGLSDWIVTSDWNVQERKG 1028
                                                                                                  1059 TSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKBGVGDGYVIIRDGANQTETLTFNICDD 1118
                                                                                                                    26;
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                                NDALPEI PGMNYTS PTELTNRLQQAWNLYDLRNA I PNGDFRNGLSDWNATSDVNVQQLSD
                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBd (Insecticidal delta-endotoxin
CrylB(d)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYLBD OR CRYLB(D) OR CRYLA1 OR CRYE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSPNNQNBYEILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSEGENPBLFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CULY. Microbiol. 40:227-232(2000).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20153386; PubMed=10688690;
Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
"Cloning of two new cry genes from Bacillus thuringlensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XYLOSTELLA.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as
                                                                                                                                                                     DTGVLSADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEER 1167
                                                                                                                                                                                         Best Local Similarity 42.0%; Pred. No. 1.4e-131;
Matches 537; Conservative 205; Mismatches 377; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.5%; Score 2445; DB 1; Length 1231; 42.0%; Pred. No. 1.4e-131;
                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis (subsp. wuhanensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=52024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1231 AA; 139654 MW; 129A0371CDDBEE52
                                                                                                                                                                                                                                                                                            PRT; 1231 AA
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InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00555; endotoxin; 1.
Pfam; PF03944; endotoxin C; 1.
Pfam; PF03945; endotoxin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U70726; AAD10292.1; -.
HSSP; P02965; ICIY.
                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toxin; Sporulation.
SEQUENCE 1231 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=HD-525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wuhanensis strain
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CIBD BACTZ
10 BACTZ
10 BACTZ
DT 30-MAY
DT 30-MAY
DT 16-OCT
DE CYPIBLO
GN CRYIBLO
GN NCBIT
RN SEQUEN
RN MEDLIN
RN MEDLIN
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RN WEDLIN
RN HASSP;
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DR HILEEPP
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                                                                           I PVVKAHTLVSGTTVI KGPGFTGGNI LKRTSSG------PLAYTSVSVKSPLSQR
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NT----AINTVVSVTGATLSALGVPGASFITNFYLKITGLLWPHDK-NIWDEFWTEVBT
                                         LIDOKI TDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDPV
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                                                                                                            | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              part of
                            1 MSPNNQNEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Payme J.M., Fu J.M.;

"Colleopteran-active Bacillus thuringiensis isolates and genes encodin colleopteran-active bacillus thuringiensis isolates and genes encodin colleopteran-active toxins.";

Patent number US5286486, 15-FEB-1994.

-!- FUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA.

-!- PETHELIAL CELLS OF COLEOPTERA.

-!- DEVELOPMENTAL STRAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: Toxic segment of the protein is located in the N-
                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry3Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1138 AA; 129658 MW; B12DC80C0A56D1DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=132267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the delta endotoxin family.
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ев 402;
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43.2%; Pred. No. 2.6e
ive 210; Mismatchee
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR0086539; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                      DQTS-----
    GDGYVIIRDGANQTETLTFNICDD
                                                                                                                                                                                       1213 GBTEGKFIVDSVELLMEB 1231
                                                                                                                                                                                                                                                                                                                                                         (Rel. 40, Created)
                                                                                                                                                                      1149 SETEGVFNIESVELVLEEE
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es 510; Conservative 2
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(Rel. 40,
crystal pr
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SEQUENCE 1138 AA
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16-0CT-2001
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Search completed: June 21, 2004, 10:10:58 Job time: 27 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

June 21, 2004, 10:10:21; Search time 90 Seconds (without alignments) 3663.699 Million cell updates/sec

US-10-089-678-1 Perfect score:

1 MSPNNQNEYELLDASSSTSV.......MSETEGVFNIESVELVLEBE 1167

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseq11980s: geneseqp1990s: geneseqp2000s: geneseqp2001s: geneseqp2002s: geneseqp2003bs: geneseqp2003bs: geneseqp2004s: A_Geneseq_29Jan04:* 1: geneseqp1980s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aau80281 Bacillus	Aar28900 Toxin 50C	Aar25997 Delta-end	Aar33768 Bt isolat	Aaw06418 Antiscara	Aar27343 B.thuring	Aar44208 Bacillus	Aar32354 Coleopter			Aau99255 Bacillus	Aaw06417 Antiscara	Aaw84581 Amino aci	Aaw84584 Amino aci	Aaw84571 Amino aci	Aaw84591 Amino aci	Aaw84575 Amino aci	Aaw84586 Amino aci	Aaw84582 Amino aci	Aaw84593 Amino aci		Aaw84578 Amino aci	Aaw84576 Amino aci	Aar48678 Insectici	Aaw84570 Amino aci
ΩI	AAU80281	AAR28900	AAR25997	AAR33768	AAW06418	AAR27343	AAR44208	AAR32354	AAR51692	AAU99256	AAU99255	AAW06417	AAW84581	AAW84584	AAW84571	AAW84591	AAW84575	AAW84586	AAW84582	AAW84593	AAW84588	AAW84578	AAW84576	AAR48678	AAW84570
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* Query Match	100.0	66.3	66.3	66.3	66.3	66.1	1.99	9.09	9.09	54.0	53.7	52.2	51.8	51.8	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7	51.7
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	Amino	Aaw84568 Amino aci	Aab82178 Cry9C #1.	Aaw84583 Amino aci	Aaw84592 Amino aci	_	. *	_	_	_	Aaw84587 Amino aci	Aaw84573 Amino aci	Aaw84567 Amino aci	•	Aaw84580 Amino aci	Aaw84574 Amino aci	_	Aay24960 Bacillus	Aau02034 B. thurin	
AAW84566	AAW84569	AAW84568	AAB82178	AAW84583	AAW84592	AAW84572	AAW84577	AAW84590	AAW84579	AAW84589	AAW84587	AAW84573	AAW84567	AAW84585	AAW84580	AAW84574	AAW46857	AAY24960	AAU02034	
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51.7	51.7	51.7	51.7	51.7	51.7	51.6	51.6	51.6	51.6	51.6	51.6	51.6	51.5	51.5	51.5	51.4	51.3	51.3	51.3	
3123	3123	3123	3123	3122	3122	3121	3121	3120	3120	3119	3118	3117	3115	3115	3114	3109	3100.5	3100.5	3100.5	
56	27	28	5	30	31	32	33	34	35	36	37	38	30	40	41	42	43	44	45	

ALIGNMENTS

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Bacillus thuringiensis insecticidal protein.
                                            Insecticide; transgenic; Coleoptera larvae.
     AAU80281 standard, protein; 1167 AA
                                                                                               03-AUG-2000; 2000JP-00236140.
                                                                                     03-AUG-2000; 2000JP-00236140.
                         30-JUL-2002 (first entry)
                                                       Bacillus thuringiensis.
                                                                 JP2002045186-A.
                                                                           12-PBB-2002.
               AAU80281;
AAU8028
```

(SDSB-) SDS BIOTECH CORP.

WPI; 2002-356468/39.

A protein having insecticidal activity, a DNA encoding said protein, and an agent and a method for preventing harmful organisms. Claim 1; Page 9-12; 19pp; Japanese.

This invention relates to a crystalline protein comprising a fully defined sequence and the nucleotide sequence encoding this protein. The cefined sequence and the nucleotide sequence encoding this protein. The protein of the invention is an agent for preventing harmful organisms comprising Bacillus thuringlensis serovar galleriae SDS502, its mutant or a microbe transformed by a DNA encoding the protein. This microbe can be used to produce a protein containing the protein, or containing a protein having insecticidal activity produced by the SDS502, its mutant or a transformed microbe which is transformed by using the above DNA, and produces the above protein having insecticidal activity, a plant or a seed transformed by using the above DNA, and Bacillus thuringiensis serovar galleriae SDS502 producing a protein comprising and producing a crotein showing insecticidal activity. The protein of the invention may have insecticidal activity. The agent is used for preventing Coleoptera larvae. This sequence represents the Bacillus thuringiensis insecticide protein of the invention

Sequence 1167 AA;

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ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVBD 120
                                                                                                                                                                                                     Spotted Spider;
                                                                                                                                                                                                                    Bacillus thuringiensis; kumamotoensis PS50C
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91US-00759248.
91US-00768141.
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                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page
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13-SEP-1991;
30-SEP-1991;
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25-MAR-2003
01-APR-1993
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                                                                                                                                                                                                                                               LPLNNTEYLEYWVGHSIKYKYTVASSALRRNYGTITSNKIKYYDLANKDIPQVRSLGADL
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                                                                                                                                                                                                                                                                                                                  RGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAHTL
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                                MSPNNQNEYE11.DASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                         ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVED
                                                                        LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDPV
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Query Match 100.0%; Score 6044; Best Local Similarity 100.0%; Pred. No. 0; Matches 1167; Conservative 0; Mismatches
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Gene sequences encoding a toxin which is active against acarides and is obtainable from B. thuringiensis isolates PS17a, PS17b, 33f2, PS52A1, PS69D1, PS8AA1 and PS50C are given in AAQ30803-07 and AAQ30802-21 respectively. The toxin is a delta-endotoxin active against acarid pests, including the Two Spotted Spider mite. The isolates can be used against non-phytophagus mites such as acarid pests of livestock, fowl and stored prods. The genes can be cloned and used to transform other hosts, which can be used to control mites, or in the case of transgenic plants, be resistant to mites. (Updated on 25-MMR-2003 to correct PN field.) 9 9 1021 QQAMILYDLRNAIPNGDFRNGLSDMATSDVNVQQLSDTSVLVIPNMNSQVSQQFTVQPN
1021 QQAMNLYDLRNAIPNGDFRNGLSDMNATSDVNVQQLSDTSVLVIPNMNSQVSQOFTVQPN 1081 YRYVIRVTARKEGYGDGYVIIRDGANQTETLIFNICDDDTGVLSADOTSYITKTVEFTPS MSPNNQNEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP YRYVLRVTARKEGVGDGYVI IRDGANQTBTLTFNI CDDDTGVLSADQTSY I TKTVRFTPS New Bacillus thuringiensis isolates and toxins - used for controlling acarid pests of livestock, fowl, stored prods. and plants. Gaps mite; phytophagus Ouery Match 66.3%; Score 4008; DB 2; Length 1157; Best Local Similarity 66.1%; Pred. No. 1.7e-255; Matches 773; Conservative 144; Mismatches 238; Indels 14;

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                                                                     AKIPSFAISGOEVPLLSVYAQAANLHLILLEDASIFGAEWGFTPGEISTFYDROVTRTAQ 240
                                                                                        240
                                                                                                                       241 YSDYCVKWYKIGLDKIKKGITISKSWLNYHQPRREMTLIVLDLVALPPNYDTHMYPLETTAQ 300
                                                                                                                                                   LTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRAG 360
                                                                                                                                                                                          LPLANTEYLEYWYGHSIKYRYT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD 419
                                                                                                                                                                                                                                LANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPPENE-P 478
                                                                                                                                                                                                                                            LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH 538
                                                                                                                                                                                                                                                                                                                TLVSGTTVIKGPGFTGGNILKRISSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT 598
                                                                                                                                                                                                                                                                                                                                                        599 ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD 658
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LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180
                                                 180
                                                                                                           YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRRBMTLLVLDLVALPPNYDTRTYPIETTAQ 300
                                                                               SSIPSFAVSGHEVLLLAVYAQAVNLHLLLLERDASIFGEEWGFTFGEISRPVNRQVQLTAB
                                                                                                                                                                                                                                                                                                                          GIWVVFKI PTTNGYATLGNLELVEBGPLSGETLERAQQQEQQWQDKWARKRGASEKAYYA
                                        KPELI PVNATPEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANLVECLSDELYP
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The sequence given is an approx. 130 kD protion known as Bacillus thuringionsis PS50C (B.t.PS50C). This novel delta-endotoxin has been shown to be active against the Colorado potato beetle (Leptinotarsa decemineata). The gene encoding this toxin can be transformed into suitable hosts such as Pseudomonas, which can then be applied to the environment of coleopteran insects where they will proliferate and be ingested by the insects. This DNA sequence can be inserted into an expression vector which contains a promoter/operator region, a ribosome binding site, polyadenylation signals, etc. This will allow transcription and translation of the cells in the appropriate host. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insecticidal Bacillus thuringiensis strain NRRL B-18746 - and DNA encoding it, vectors and transformed cells, effective against
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                                                                                                                                                                                                                                                                                                                                                                             potato beetle, Leptinotarsa decemlineata,
1129 PYTDQMWIRISETEGFFYIESVELIVDVB 1157
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                                                                                                                                  AAR25997 standard; protein; 1157
                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas; expression vector
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                                                                                                                                                                                                                                              (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringiensis.
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                                                                                                                                                                                                                                                                                                                             Delta-endotoxin.
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27-JAN-1993
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                                                                                                   AAR25997
ID AAR2
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toxin; Ti; Ri; plant; cell;

91US-00758020 92US-00941650 92WO-US007697

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Controlling lepidopteran pests - using compsn. of Bacillus thuringlensis strains or plants or microorganisms transformed with their toxin genes.
                                                                                                                                                                                                                                                   Claim 12; Page 22-25; 38pp; English
15-JUL-1993 (first entry)
                                                     Bacillus thuringiensis
                                                                                                                                                                           KA, Bradfish GA
                                   Lepidopteran-active;
                                                                                                                                                        (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                             WPI; 1993-100566/12.
                                                                                                                                                                                                      N-PSDB; AAQ38653
                                                                                                            11-SEP-1992;
                                                                                                                              12-SEP-1991;
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                  Bt isolate
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                                                       YLGDTIEKORFUKTMDNGASLITYETFREASFITDEQFRETQDKILLSMGDFSSGQEVYID
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                                             LTREVYTOPI VFNRETSGGFCRRWSLNSDISFSBVESAVIRSPHLPDILSEIBFYTTRAG
                                                                                  LPLANTEYLEYWYGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD
                                                                                           LANYYAQVYGVPYAS FTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPENB-P
                                                                                                                                                        LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH
                                                                                                                                                                                                                                 ISGIRIYSINVNKTMNKGDDLIFNTFDLATIGTAFTFSNYSDSLIVGADSFASGGEVYVD
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The sequences given in AAR33768-70 represent lepidopteran-active toxins. The DNA encoding these sequences were used within a Ti or Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning Backiluus thuringiensis (Bt) . It may then be applied directly to the plant locus (Updated on 25-NAR-2003 to correct PN field.) (Updated on 25-NAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTMQVCTQNYNTIDEIPPENB-P 478
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                                                                                                                                                                                                           MSPNNQNEYE1LDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                Gaps
                                                                                                                                                                                14;
                                                                                                                                                    Length 1157;
                                                                                                                                                                                Indele
                                                                                                                                                   Ouery Match 66.3%; Score 4007; DB 2; Best Local Similarity 66.1%; Pred. No. 1.9e-255; Matches 773; Conservative 144; Mismatches 238;
                                                                                                                            Sequence 1157 AA;
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protein; 1157

standard;

AAR33768

AAR33768

RESULT

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AAR33768

(revised)

25-MAR-2003

Michaels TB;

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Narva

91US-00808316. 92US-00828430. 93US-00014941.

us-10-089-678-1.rag

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The DNA encoding this sequence was isolated from the Bacillus acarab pests.

The DNA encoding this sequence was isolated from the Bacillus are funtinglensis strain knumamotoensis. Insects in the family Scarabaeidae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses, playing fields and lawns. The larvae of many species also attack grains, there is grubs, and conmaentals. The larvae are known as white grubs, or chafter grubs, and cnamentals. The larvae are known as white grubs, or chafter grubs, and can be found in decaying organic matter, or in the soil where they consume plant roots. In Burope and the U.S. populations of these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. These toxin sequences, and intext cells that are capable of expressing these proteins, can be used to control many pests of the family scarabaeidae, such as species of cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                      New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult
                                                                                                                                                                                    Example 2; Col 21-26; 24pp; English.
                                                                                                                                                                their larvae.
                                                        (MYCO ) MYCOGEN CORP
                                                                                                     WPI; 1996-424659/42.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1157 AA;
                                                                                                                 N-PSDB; AAT43222.
                                                                               Foncerrada L,
           16-DEC-1991;
30-JAN-1992;
01-FEB-1993;
                                                                                                                                                              pests and
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LANYYQKAYGVPGSWPHMVKR--GTSSTTAYLYSKTHTALQGCTQVYESSDEIPLDRTVP 477
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                                                                                                                               LSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAH
                                   TLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTINLRLFVT
                                                                                                                ISGTRIYSINVNKTMNKGDDLTPNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
                                                                                                                                                             NEXRMINDAVKBAKRLVQARNLLQDTGFNRINGENGWTGSTGIEVAEGDVLFKDRSLRLT
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(first entry)
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                         Gaps
                       14;
Length 1157;
Query Match
Best Local Similarity 66.1%; Pred. No. 1.9e-255;
Matches 773; Conservative 144; Mismatches 238; Indels
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control;

Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest contro larval stage insect; grain; tuberous crop; white grub; chafer grub; cyclocephala; popillia.

Bacillus thuringiensis; strain kumamotoensis

US5554534-A 10-SEP-1996 94US-00315468

30-SEP-1994;

and

Ë Payne

Sick

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Foncerrada L,
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                                                             TLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                                                                                                       ISGTRIYSINVNKTWNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVD
                                                                                                                                                                                   KPELI PVNATPEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANLVECLSDBLYP
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02-JAN-1992;
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LTREVYTOPIVPNRETSGGPCRRWSLASDISPSKVESAVIRSPHLPDILSBIEFYTTRAG 360
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                                                                                                                                                                                                                                                                                                                                        SIPSPAVSGHEVILLAVYAQAVNLHILLILRDASIFGEEMGFTPGEISRFYNRQVQLTAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIBTTAQ
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                                                                                                                                                                                                                                         Gaps
                                                               DNA
                                                                                                                                                                                                                                         14;
                                                               toxin,
                                                                                                                                                                                                                Length 1157;
                                                              New Bacillus thuringiensis isolate - used for preparing to transformed hosts for controlling coleoptera insect pests.
                                                                                                                                                                                                                                         Indele
                                                                                                                                                                                                            Ouery Match 66.1%; Score 3995; DB 2; Best Local Similarity 66.0%; Pred. No. 1.2e-254; Matches 771; Conservative 145; Mismatches 239;
                                                                                                      Claim 12; Page 18-20; 33pp; English.
Ä,
                        WPI; 1992-323784/40
                                                                                                                                                                                    Sequence 1157 AA;
                                      N-PSDB; AAQ28940
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                                                                    Query Match 66.1%; Score 3994; DB 2; Best Local Similarity 66.0%; Pred. No. 1.4e-254; Matches 771; Conservative 144; Mismatches 240;
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                                                                                                                                                    and
                                                                                    DNA encoding the insecticidal toxin can be cloned into baculo viruses an transferred to other host microbes, preferably E. coli NN522 (pWYC 2320) NRRL B-18769, to control acaride peste, or to plants which become resistant to the acaricide peste. Specifically, the two-spotted spider mite (Tetranychus urticae) is controlled. (Updated on 25-MAR-2003 to
LLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFSPHIDTGEIDLNENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Controlling acaride pests e.g. two spotted spider mite - utilising Bacillus thuringiensis delta-toxins cloned into microbe hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crystal protein; delta endotoxin; acaricide; pesticide;
biological control agent; transgenic plant; crop improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus thuringiensis serovar kumamotoensis; (isolate PS50C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The protein sequence is that of a toxin active against Coleoptera that is produced from a pure culture of Bacillus thuringiensis serovar japonesis variety Buibui (FERM BP-1465). The toxin is a delta-endotoxin which has a mol. wt. of ca. 130 kD. It is useful for control of coleoptera larvae e.g. it is effective against Anomala cuprea but has little effect on Lepidoptera. The toxin can be used as B.t. spores or crystals, as opt. treated cells (B.t. or transformed microorganisms) or it is expressed by plants. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Delta-endotoxin; larvae; Anomala cuprea; spore;
thuringiensis; virus; insect; FERM BP-3465.
                                                                                                                                                                                                    PSTEQVWIDMSETEGVFNIBSVELVLEEE 1167
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  1047 QQLSDTSVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKGGVGGYVIIRDGANQTETLTF 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTFISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNMLENRNDTRARSVVVTQYIALELDF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This insecticidal protein has activity against Coleopteran insect larvae and has been isolated from Bacillus thuringiensis serovar japonensis strain Buibui. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAKIPSFAISGGEVPLLSVYAQAANLHLLLKBASIFGABWGFTPGBISTFYDRQVTRTA
                                                                                                                                                                                                                                                 751. .766
/note= "amino acids 751-766 are not given in the
specification and so have been decoded from AAQ58975"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           DNA from Bacillus thuringiensis serovar - useful in insecticides against Coleoptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.6%; Score 3662.5; DB 2; Length Best Local Similarity 63.8%; Pred. No. 1.1e-232; Matches 752; Conservative 109; Mismatches 257; Indels
                                                                                                                                                                  B.thuringiensis serovar Japonensis insecticidal protein
                                                                                                                                                                                    insecticidal protein; Coleoptera larvae; Buibui fungus
                    Bacillus thuringiensis; (serovar Japonensis strain Buibui).
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                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 9-13; 18pp; Japanese.
                                                                                           AAR51692 standard; protein; 1149
                                                                                                                                                                                                                                                                                                                                 92JP-00213886
                                                                                                                                                                                                                                                                                                                                                      92JP-00213886
                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                      Japonensis strain Buibui
                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                          (KUBI ) KUBOTA CORP.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-121220/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ58975
                                                                                                                                                                                                                                                                                           JP06065292-A
                                                                                                                                                                                                                                                                                                                                 11-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                      11-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                            Insecticidal
                                                                                                                                   16-OCT-2003
04-NOV-1994
                                                                                                                                                                                                                                                                                                              08-MAR-1994
                      1114
                                       1107
                                                                                                                AAR51692;
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1048 TSDVNVQQLSDTSVLVIPNANSQVSQOFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQ 1107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GETLERAQQQEQQWQDXMARKRGASEXAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAA 987
S--ISSARYIRHWAGHQISYHRIPSDNIIKQMYGTNONLHSTSTPDFTNYDIYKTLSKDA 414
                                                                                     -----TLKYNPVSK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest; Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cry1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIAGTRDSELELPPETSDQPNYESYSHRLCHITSIPATGSTT-----GLVPVPSWTHRS
                                                                                                                                                                                            ADVINIVYSDKITQIPVVKAHTL---VSG---TTVIKGPGFTGGNILKRISSGPLAYTSV
                                                                                                                                                                                                               TRTLTRNICDDDT-GVLSA------
                                                                                                                                                                                                                                                                     SVK-SPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIG
                                                                                                                                                                                                                                                                                   SKIDALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLKGFIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENNGENGNMSSDSHAPSFHIDTGBIDLNENTGIWVVFKIPTTNGYATLGNLELVBEGPLS
                                                     DLAN-----YYAQVYGVPYASFTLLDK--NTGSGSVGGPTYSKPHTTMQVCTQNYNTID-
                                                                                                                        -----BIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRS
                                                                                                                                                                                                                                                                                                                                         TAPTFSNYSDSLTVGADSFAS - - - GGEVYVDKPELI PVNATPEABEDLDVAKKAVNGLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RINGENGWICSTGIEVAEGDVLFKORSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis Cryl218-1 protein sequence.
                                                                           | : ::: | : :|:| 415 VLLDIVFPGYTYIPFGMPEVBFPMVNQLNNTRK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ETPIS-SSTVOTGIGIVGQVLGALGVPFAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 DLIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OYSDYCVKWYNTGLDKLKGTWAASWLKYHOFRREMTLLVLDLVALPPNYDTRTYPIETTA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QLIREVYIDPIVFNRETSGGPCRRWSLNSDISPSEVESAVIRSPHLFDILSEIEFYTIRA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLPLANTEYLEYWVGHSIKYRNTNASSALERNYGTITS-NKIKYYDLANKDIPQVRSLGA 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                    pest e.g.
                                     Pesticidal, spraying, dusting, broadcasting, seed coating, insect pest, Colorado potato beetle, western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cry1218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSPNNQNEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VAKIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated pesticidal polypeptide useful for impacting insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 54.0%; Score 3263.5; DB 5; Length 1210; al Similarity 53.4%; Pred. No. 2.6e-206; 667; Conservative 178; Mismatches 284; Indels 119;
                                                                                                                                                                                                                                                                                                                                             Ë
                                                                                                                                                                                                                                                                                                                                             Sims
                                                                                                                                                                                                                                                                                                                                             Kahn TW,
     Bacillus thuringiensis Cry1218-2 protein sequence.
                                                                                                                                                                                                                                                                                                                                           Flannagan RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 103-105; 176pp; English
                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                    24-OCT-2000; 2000US-0242838P.
23-OCT-2001; 2001US-00032717.
                                                                                                                                                                                                                   24-OCT-2001; 2001WO-US045468
                                                                                                                                                                                                                                                                                                                                           Peng X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colorado potato beetle.
                                                                                                         Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                              2002-519178/55.
                                                                                                                                                                                                                                                                                                                                           Duck NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 667; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endotoxin protein
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                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK87235.
                                                                                                                                            WO200234774-A2
                                                                                                                                                                               02-MAY-2002
                                                                                                                                                                                                                                                                                                                                             Abad AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360
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The present invention relates to a new pesticidal polypeptide. The molecules of the impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a Bacillus thuringiensis wild-type Cryl218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLTREVITOPLGAVNVSSIG---SW-YDXAPSFGVIESSVIRPPHVFDYITGLTVYTOSR 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S--ISSARYIRHWAGHQISYHRVSRGSNLQQMYGTNQNLHSTSTFDFTNYDIYKTLSKDA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLAN-----YYAQVYGVPYASFTLLDK--NTGSGSVGGFTYSKPHTTMQVCTQNYNTID- 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLIRBVYTDPIVPNRRISGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBPYTTRA 359
                                                                                                                                                                                                                                                                                       pest e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRRREMTLLVLDLVALPPNYDFRTYPIETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETFIS-SSTVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLPLINITEYLEYWYGHSIKYKNINASSALERNYGTITS-NKIKYYDLANKDIFOVRSLGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                            New isolated pesticidal polypeptide useful for impacting insect Colorado potato beetle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1206;
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                                                                                                                                                                                                             Simg
                                                                                                                                                                                                             Kahn TW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 53.7%; Score 3246.5; DB 5; Best Local Similarity 53.4%; Pred. No. 3.4e-205; Matches 665; Conservative 172; Mismatches 290;
                                                                                                                                                                                                          Flannagan RD,
                                                                                                                                                                             (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 96-98; 176pp; English
                                                                                                                               24-OCT-2000; 2000US-0242838P.
23-OCT-2001; 2001US-00032717.
                                                                                                   24-OCT-2001; 2001WO-US045468
                                                                                                                                                                                                          Abad AR, Duck NB, Feng X,
              Bacillus thuringiensis.
                                                                                                                                                                                                                                        2002-519178/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endotoxin protein
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                                                                                                                                                                                                                                                       N-PSDB; ABK87234
                                          WO200234774-A2
                                                                       02-MAY-2002
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                                                                    ADLNITIYSDKITQIPAVKCWDNLPFVPVVKGPGHTGGDLLQYNRSTGSVGTLFLARYGL
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                                                                                                                                       ---TPSNYSDSLTVGADSPAS-GGEVYVDKFBLIPVNATFEABBDLDVAKKAVNGLFTSK
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                    ---BIPPB--NBPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRS
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larval stage insect; grain; tuberous crop; white grub; chafer grub;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTFNICDDDT-GVLSA-----
415 VLLDIVYPGYTYIFFGMPEVEFFMVNQLNNTRK---
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(first entry)
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                  AS - - TINLALP - VIISGTRIYSINVNKT - MNKGD - DLIFNIFDLATIGTAPTPSNYSDSL
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                                                            DEIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVYSD
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ESVELIVDVB 1169
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Synthetic.
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                                                                                                                                                                                                                                                            w nucleic acid encoding B.thuringiensis toxin active against scarab(s) also related toxin and transformed microbes, effective against adult
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Local Similarity 54.0%; Pred. No. 5.7e-199;
hes 653; Conservative 179; Mismatches 294;
                                                                                                                                                                             Michaels TE;
                                                                                                                                                                                                                                                                                                                          Claim 2; Col 29-36; 24pp; English.
                                                                           91US-00808316.
92US-00828430.
93US-00014941.
                                              94US-00315468
                                                                                                                                                                           Foncerrada L, Narva KB,
                                                                                                                                                                                                                                                                                           pests and their larvae
                                                                                                                                            (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                            WPI; 1996-424659/42.
N-PSDB; AAT43221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1169 AA;
                                                                                            30-JAN-1992;
01-FEB-1993;
                                            30-SEP-1994;
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               10-SEP-1996
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                                                                                                                                                                           New Bacillus thuringlensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia mubilalis, Heliothis virescens and Diatraea
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                                                  25-JUN-1998;
                                                                          27-JUN-1997;
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1005 IPGENYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                                                               ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
                                                                                                                                                                     PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
                                                                                                                                                                                                                                                    593 LRLFVIISGTRIYSINVNKTMNKGDDLIFNTF---DLATIG---TAPTFSNYSDSLTVGA
                                                                                                                                                                                                                                                                                                                                        DSPASGGEVYVDKFBLIPVNATPEAEEDLDVAKKAVNGLPTSKKDALQTSVTDYQVNQAA
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GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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1005 IPGMNYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                                                                                 FSIRVIAGGUSIGDVALGSTWONEGGELTYBSPFTREPTTTTGPNPPFTFTQAQBILTVNA
                                                                                                                                                                                                                                                                                                                                NLVECLSDELYPNEKRALMDAVKAAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA
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GADLANYYAQVYGVPYASFTL---LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
                                                                           ENEPLSRGYS-HRISHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239
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                                                                                                                                                                                                                                                      or producing transgenic plants in controlling pest insects, Ostrinia nubilalis, Heliothis virescens and Diatraea
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                                                                                                                  (PLBZ ) PLANT GENETIC SYSTEMS
                                        98WO-EP004033
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                                                                               27-JUN-1997;
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This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing more transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured cells of the transgenic plants and used in insecticide compositions against lepidopteran insects, especially Ostrinia mubilalis, Heliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. CryB-type protein), and used to transform B-thuringiensis which produces other insecticidal toxins. Such strains are useful against a produces other insecticidal toxins. Such strains are useful against a variety of insect peats, or insects where insect resistance development is prevented or delayed. (Noce: this sequence is not given in the cryonic or specification, but is generated using the information provided by the
                                                                                                                                                                                                New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea grandiosella.
                                                                                           GENETIC SYSTEMS NV
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98WO-EP004033
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  25-JUN-1998;
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                                                                                                                                         Roeck S,
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Query Match 51.7%; Score 3126; DB 2; Length 1157; Best Local Similarity 52.3%; Pred. No. 2.9e-197; Matches 619; Conservative 195; Mismatches 327; Indels 42. Sequence 1157 AA;

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240 119 OYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTA 299 QLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIEFYTTRA 359 360 GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416 417 GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP 474 9 1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDQTTTLQNWNYKDYLRMSEGENPELFGNP 61 ETPISS-STVQTGIGIVGQVLGALGVPPAGQIASPYSFIVGQLMPSSTVSVWEMIMKQVE DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLRNRNDTRARSVVVTQYIALELDP VAKI PSFAI SGOEVPLLSVYAQAANLHLLLLRDAS I FGAEWGFTPGEI STFYDRQVTRTA 241 120 121 181 300 301 240 360

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MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004 1005 IPGWNYTSPTELTWRLQQAMNLYDLRNAIPNGDFRWGLSDWNATSDVNVQQLSDTSVLVI 1064 1065 PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLS 1124 SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHHQETLTFNACDYDVNGTY 1114 638 874 592 578 646 706 698 764 824 884 PHIDTGBIDIMENTGIWVVFKIPTTNGYATLGMLELVBEGPLSGBTLERAQQQEQQWQDK 944 SYINTGDLNASVDQGIWVVLKVRTTDGYATLGNLELVEVGPLSGESLEREQRDNAKWNAE 934 461 DE---STGSSTHRISHVTFFSFQTNQAGSIANAGSVPTYVWTRRDVDLANTITPNRITOL 815 HHKVHLVKNVPDNLVSDTYSDGSCSGINRCDEQHQVDMQLDAEHHPMDCCEAAQTHEPS -- CRDLYDTNDELPP PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN 593 LRLPVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA DSFASGGBVYVDKFELIPVNATFEABEDLDVAKKAVNGLFTSKXDALQTSVTDYQVNQAA NLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA RHRANGIVICAVPDNILLPDVLPVNSCGIDRCSBQQYVDANLALENNGENGNMSSDSHAFS ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITOI 1125 ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIBSVELVLEBE 1167 414 AVDFRSALIGIYGVNRASFVPGGLFNGTTSPANGG----462 533 519 647 639 707 669 765 759 825 945 475 셤 ठे გ ઠે 셤 ઠે 셤 8 셤 è 셤 ሯ a ሯ 셤 ઠ 셤 ð 8 6 કે ద Š 셤

completed: June 21, 2004, 10:14:49 time Search gg

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Sequence 63, Appl
Sequence 23, Appl
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(without alignments)
819.552 Million cell updates/sec
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Sequence 4,
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US07_REW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-013-717-4

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US-10-606-320-4

US-10-032-717-2

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US-10-428-961-63
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Listing first 45 summaries
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Sequence 1, Application US/10089678;
Sequence 1, Application US/10089678;
Publication No. US20030017967A1
GENERAL INFORMATION:
APPLICANT: ASANO, Shinichiro
TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE PROTEIN,
TITLE OF INVENTION: NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REPRENCE: G68821
CURRENT PELLING DATE: 2002-05-02
FRIOR APPLICATION NUMBER: US/10/089,678
CURRENT FILING DATE: 2000-08-03
FRIOR FILING DATE: 2000-08-03
FRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                      Sequence 10, Appl
Sequence 12, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 34, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 39, Appl
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Sequence 12, A
Sequence 14, A
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Sequence 12,
 Sequence 38,
Sequence 2,
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US-09-873-873-10

US-09-873-873-114

US-09-873-873-12

US-09-873-873-14

US-09-97-914-12

US-09-97-914-12

US-09-97-914-14

US-10-365-645-10

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100.0%; Pred. No. 0;
tive 0; Mismatches
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; OKGANISM: Bacillus thuringiensis
US-10-089-678-1
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Matches 1167; Conservative
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Best Local Similarity
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APPLICANT: Andre R. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Ranald D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
TITLE OF INVENTION: Genes Encoding No. US20020151709Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT FILING DATE: 2001-10-23
FRIOR APPLICATION NUMBER: 60/242,838
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSRQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         518 ADVINTVYSDKITQIPVVKAHTL---VSG---TTVIKGPGFIGGNILKRISSGPLAYTSV 571
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                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                  Length 1210;
                                                                                                                                                                                                                                                                                                                                                                 667; Conservative 178; Mismatches 284; Indels 119;
                                                                                                                                                                                                                                                                                                                                    DB 13;
                                                                                                                                                                                                                                                                                                                                    54.0%; Score 3263.5; DI 53.4%; Pred. No. 3e-258;
                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Bacillus thuringiensis
Publication No. US20020151709A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                            LENGTH: 1210
                                                                                                                                                                                                                                                                                                       US-10-032-717-4
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Best Local S
Matches 667
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                                                                       YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIBTTAQ
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APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Naves Encoding No. US20030177528A1el Proteins With
ITLE OF INVENTION: Genes Encoding No. US20030177528A1el Proteins With
ITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE OF INVENTION NUMBER: US/10/414,637
CURRENT PILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR PILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
 PPIKFTTTEPFITLGAIFEAEDFLGIEAYIDRIBFIPVDETYEAEQDLEAAKKAVNALFT 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/10414637; Publication No. US20030177528A1; GENERAL INFORMATION:
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1103 TETLIFSASDYDTNGAYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASSNTNGYN 1162
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                                                                                                                                                                            ADVINITY/SDKITQIPVVKAHTL ---VSG---TTVIKGPGPTGGNILKRTSSGPLAYTSV
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Publication No. US20020151709A1
Publication No. US20020151709A1
Publication No. US20020151709A1
PUBLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Nicholas B. Duck
APPLICANT: Ronald D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lannagan
APPLIC
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1103 TETLTFSASDYDTNGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASNTNGYN 1162
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Best Local Similarity 53.4%; Pred. No. 3e-258;
Matches 667; Conservative 178; Mismatches 284; Indels 119;
                                                                                                         US-10-800-320-4
; Sequence 4, Application US/10606320
; Publication No. US20040091505A1
; GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Refael Hermann
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: James R. Presnail
APPLICANT: James R. Presnail
APPLICANT: James R. Presnail
APPLICANT: James R. Wong
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REPERCE 35718/263948
CURRENT FILING DATE: 2003-06-25
FRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2003-04-04
NUMBER OF SEG ID NOS: 134
SOSTIBARE FESTERCE FOR Windows Version 4.0
SEG ID NO 4
SEG ID NO 4
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1101 TLTFSASDYDTHGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASNTNGYNTN 1160
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10414637
; Sequence 2, Application US/10414637
; Bublication No. US20030177528A1
; GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Aisholas B. Duck
APPLICANT: Aisholas B. Duck
APPLICANT: Theodore W. Rahn
APPLICANT: Theodore W. Rahn
APPLICANT: Lynn B. Sims
TITLE OF INVENTION: Genes Encoding No. US20030177528A1e1 Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/23708
FILE REPERENCE: 35718/23708
CURRENT APPLICATION NUMBER: US/10/032,717
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                   TLTPNICDDDT-GVLSA----- 1125
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                                                                                                                                                                                                                                                                                                                             ----DQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEB 1167
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Matches 665; Conserv
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                                                                                                                                                    DB 13; Length 1206;
                                                                                                                                                   Query Match 53.7%; Score 3246.5; DB 13; Length 1206
Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indela 119;
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                   ; ORGANISM: Bacillus thuringiensis US-10-032-717-2
                                                                               LENGTH: 1206
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                                           S--ISSARYIRHWAGHQISYHRVSRGSNLQQMYGTNQNLHSTSTFDFTNYDIYKTLSKDA
                                                                                                              | : | : | | | | 415 VŁŁDIVYPGYTYIPPGMPEVBFWVNQŁNNTRK------TLKYNPVSK
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Rorald D. Flannagan
APPLICANT: Refael Herrmann
APPLICANT: Refooder W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: James K. Presnail
APPLICANT: James F. H. Wong
APPLICANT: James F. H. Wong
APPLICANT: Gao-Guo Yu
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/265948
CURRENT APPLICATION NUMBER: 08/10/606,320
CURRENT PILING DATE: 2003-06-25
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 134
NUMBER OF SEQ ID NOS: 134 ; ORGANISM: Bacillus thuringieneis US-10-606-320-2 LENGTH: 1206 61 120 121 360 357 512 61 TYPE: PRT SOFTWARE: 1 SEQ ID NO 2 ઠે 셤

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                                                                                                                                                                           Query Match 51.3%; Score 3100.5; DB 14; Lengt Best Local Similarity 52.0%; Pred. No. 6.9e-245; Matches 615; Conservative 196; Mismatches 330; Indels
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/002,285

PILING DATE: -Unknown:

PILING DATE: 1.-UL-1997

APPLICATION NUMBER: US 08/674,002

PILING DATE: 1.-UL-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sanders, Jay M.

REGISTRATION NUMBER: 39,355

REFERENCE/DOCKET NUMBER: MA-701C2

TELEPHONE: (352) 375-800
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 72: US-10-099-285-72
                                                                                                                                                                                                                        INPORNATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
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TLTFSASDYDTNGWYNTQVSNTNGYNTNNAYNTQASSTNGYNANNWYNTQASNTNGYNTN 1160
   ALEKAGKYRVRLRYATDADIVLHVNDA----QIQMPKTWNPGEDLTSKTFKVADAITTL 626
                                                 ---TPSNYSDSLTVGADSFAS-GGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSK 689
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                                                                                                             MGENGWIGSTGIBVARGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKL
                                                                                                                                                                                                                                         KGPIGSSQDLBIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALEN
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Galnesville
STATE: Plorida
COUNTRY: USA
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TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-War-2002
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 72, Application US/10099285; Publication No. US20030105319A1; GENERAL INFORMATION: Schnepf, H. Ernest Micker, Carol Natvar, Renneth B. Walz, Michelle Stockhoff, Brian
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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61 SLSISGRDAVQTALTVVGRILGALGVPFSGQIVSFYQFLLNTLWPVNDTAIWEAFMRQVB 120
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                         120 DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDP
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Sequence 28, Application US/10428961

publication No. US20030237111A1

GENERAL INPORMATION:

APPLICANT: Baun, Chih-Rei

APPLICANT: Chu, Chih-Rei

APPLICANT: Glimer, Amy J.

APPLICANT: Glimer, Amy J.

TITLE OF INVENTION: Delynuclectides, Compositions, and Methods of Use (Amended)

FILE REFERENCE: MECOZO1-1

CURRENT APPLICATION NUMBER: US/10/428,961

CURRENT APPLICATION NUMBER: 09/661,322

PRIOR FILING DATE: 1999-09-13

PRIOR FILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SEQ ID NO 28

LENGER IN 1156

LENGER IN 1156
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                                     LVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAE
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larity 52.0%; Pred. No. 6.9e-245;
Conservative 196; Mismatches 330; Indels 41;
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Matches 615; Conserv
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US-10-428-961-28
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1012 SFTELTURLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQV 1071
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LFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT Schnepf, H. Brnest
Wicker, Carol
Narva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSER: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Plorida
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COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099, 285
FLING DATE: 15-Mar-2002
CLASSIPICATION: <Unknown>
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APPLICATION NUMBER: 09/002,285
FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 32606
COMPUTER READABLE FORM:
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VKAYELSSCATVVKGPGFTGGDVIRRTNTGGFGAIRVSVTGPLTQRYRIRPRYASTIDFD 580
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                                                                                                                     APPLICANT: Arnaut, Greta
APPLICANT: Arnaut, Greta
APPLICANT: Domme, Nicole
APPLICANT: Damme, Nicole
APPLICANT: Damme, Nicole
APPLICANT: Mathieu, Eva
APPLICANT: Wathieu, Eva
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Wanneste, Usole 1,524
CURRENT PILING DATE: 2000-12-19
PRIOR PILING DATE: 2000-12-19
PRIOR PILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
SEQ ID NO 6
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47.7%; Score 2884.5; DB 15; Length 1152;
Best Local Similarity 49.1%; Pred. No. 3.8e-227;
Matches 578; Conservative 200; Mismatches 365; Indels 33;
                                                                       ; Sequence 6, Application US/10614524; Publication No. US20040016020A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-614-524-6
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1049 HWDAQVSQQFRVQPNCKYVLRVTAKKVGNGDGYVTIQDGAHHRBTLTFNACDYDVNGTHV 1108
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                                                                                                                                                                                                                                                                                                                                                                                                   NWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSA 1125
                                                                                                                                                                                                                                                                  946 ARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNLVQSIPYVYNDALPBI 1005
                                                                                                                                                  886 HIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVBEGPLSGETLERAQQQEQQWQDKM 945
                                                                                                                                                                                                                                                                                                                                                    HRANQI VKNVPDNLLPDVLPVNSCGGI DRCSEQQYVDANLALENNGENGNMSSDSHAFSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ||||| : | | || :|:::||||| ||:|:|: || NDNSYITKELVFYPKTEHMWVEVSETEGTPYIDSIBFIETQE 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wicker, Carol
Narva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/002,285
FILING DATE: «Unknown»
APPLICATION NUMBER: US 08/686,615
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
PLING DATE: 15-Mar-2002
CLASSIFICATION: <u >un current</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 76, Application US/10099285
Publication No: US20030105319A1
GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Gainesville
STATE: Florida
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-099-285-76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LELDFVAKIPSFAIS-GQE---VPLLSVYAQAANLHLLLLRDASIFGAEWGFTFGEISTF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALPPNYDT 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351 EIEFYTTRAGLPLNNTBYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDI 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIA 174
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                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                    Query Match 46.7%; Score 2825.5; DB 14; Lengt
Best Local Similarity 48.6%; Pred. No. 2.6e-222;
Matches 574; Conservative 197; Mismatches 364; Indels
APPLICATION NUMBER: US 08/886,615
PILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANGERS, Jay M.
REGISTRATION NUMBER: 39,355
REPERENCE/DOCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-6100
TELEPHONE: (352) 372-6800
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 74: US-10-099-285-74
                                                                                                                                                                                                                     LENGTH: 1150 amino acids
                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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                                                               PADYODOXINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAMNL
                                                                                                                                           SCGGIDRCSEQQYVDANLALENNGB-NGNMSSDSHAPSPHIDTGBIDLNBNTGIWVVPKI
                                                                                                                                                                                          YDLRNA I PNGDFRNGLSDWNA TSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANT APPLICATION DATA:
PEPLICATION NUMBER: US/09/988,462
PILING DATE: 20-No. US20030046726A1-2001
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-5EP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology,
STREET: 3054 Cornwallia Road
CITY: Research Triangle Park
STATE: NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-18805I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meige, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                    SVNETEGAFHIDSIEFVETER 1134
                                                                                                                                                                                                                                                                                                                                                                                                                        DMSETEGVFNIESVELVLEBB 1167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION
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US-09-988-462-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWSLNSDISFSEVESAVIRSPHLFDILSEIEFYTTRAGLPLNNTEYLEYWVGHSI--KYK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 ASGPITVLRRNYGSTTS-IVNYFSPNDRDVYQINTRSHTGLGFQN--APLFGITRAQF-- 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 LDKONTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIP--PENEPLSRGYSHRLSHITSYSF 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTEF 787
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                                                                                                                                                                                                                                                                                        4 NPNINECIPYNCLSNPEVEVLGGERGNVRT----GLQTGIDIVAVVGALGGFVGGILT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLRDASIFGAEWGFTPGEISTFYDROV-TRTAQYSDYCVKWYNTGLDKLKGTNAASWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610 NKTWNKGDDLIFNIFDLAIIGTAFIFSNYSDSLIVGADSFASGGEVYVDKFELIPVNAIP
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      62;
                                                                                                                                                                                                        Length 1134;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                       Query Match
44.8%; Score 2710; DB 14;
Best Local Similarity 48.1%; Pred. No. 7.9e-213;
Matches 559; Conservative 195; Mismatches 345;
                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 76:
US-10-099-285-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                               LENGTH: 1134 amino acids
                                                                                                 TYPE: amino acid
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ORGANISM: Bacillus thuringiensis
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                                                                                                        Query Match 41.7%; Score 2519.5; DB 10; Length 1207; Best Local Similarity 44.3%; Pred. No. 3.9e-197; Matches 548; Conservative 178; Mismatches 372; Indels 139; Gaps
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                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
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US-10-428-961-63

US-10-428-961-63

Sequence 63, Application US/10428961

Publication No. US20030237111A1

GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Gluer, Amy J.

APPLICANT: Gluer, Mark J.

APPLICANT: Rupar, Mark J.

TITLE OF INVENTION: Polynucleotides, Compositions, and Methods of Use (Amended)

FILE REPERENCE: MECO201-1

CURRENT APPLICATION NUMBER: US/10/428,961

FRIOR PILING DATE: 2000-09-13

PRIOR APPLICATION NUMBER: 60/153,995

FRIOR PILING DATE: 1999-09-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE PARENT IN VERSION 3.2

SEQUENCE: AND APPLICATION NUMBER: 00/153,995

SOFTWARE PARENT P
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                                                                                   WVVPKI PTTNGYATLGNLELVBEGPLSGBTLERAQQQEQQWQDKMARKRGASEKAYYAAK
813 VESPIGRCGEPNRCA--PHFEWNPDLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGV
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LTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHL/FDILSBIEFYTTRAG 360
                                                                 LPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDIFQVRSLGADL 420
                                                                         405 ILLITPVNGVPWARFNW--RNPLNSLRGSLLYTIGYT--GVGTQLFDSETELPPETTERP 460
                                                                                                                                LSRGYSHRLSHITSYSFSKNASSPARYGN---LPVFAWTHRSADVTNTVYSDKITQIPVV 535
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                                                                                                                                        656 YVDKFBLIPVNATFEAEBDLDVAKKAVNGLFTSKKD-ALQTSVTDYQVNQAANLVECLSD
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                                                                                                                                                                 Encoding Pesticidal Toxins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Toxin encoded by synthetic B.t. gene US-09-826-660-23
                                                                     GENERAL AREVCEATION.

APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Marya, Kenneth B.
FILE REFERENCE: Ma-714XC2D1
CURRENT APPLICATION WUMBER: US/09/826,660
CURRENT APPLICATION WUMBER: 09/178,252
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR PILING DATE: 1998-10-23
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-30-02
PRIOR PILING DATE: 1998-30-02
PRIOR PILING DATE: 1998-30-02
SOFTWARE: PATENTIN UNWBER: 60/065,215
PRIOR PILING DATE: 1998-30-02
SOFTWARE: PATENTIN UNCHER: 60/076,445
SEQ ID NOS: 27
SOFTWARE: PATENTIN UNCHER: 1998-30-02
SEQ ID NOS: 27
SEQ ID NO 23
     US/09826660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
Sequence 23, Application US; Patent No. US20010026940A1; GENERAL INFORMATION:
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                           903 NIVYKBAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIRBAYLPELSVIPGVNAAI 962
         833 KNVPDNLLPDVLPVNSCGCIDRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEI 892
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Search completed: June 21, 2004, 10:23:47 Job time : 417 secs

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PSOURCE FROM N.A.

SEQUENCE FROM N.A.

A SEAND S., Yamamoto T.;
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B seano
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29338;
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Pred. No. 0;
0; Mismatches
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Q9 573 S
Q9 4573 S
Q9 473 S
Q9 874 S
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Best Local Similarity 97.9
Matches 1143; Conservative
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Compugen Ltd
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                                       GenCore version (c) 1993 - 2004
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Shevelev A.B., Svarinsky M.A., Karasin A.I., Kogan Y.N.,
Chestukhina G.G., Stepanov V.M.;
Primary structure of the cryX**-the novel Delta-endotoxin-related
gene from Bacillus thuringiensis ssp. galleriae.";
FERS Lett. 336:79-82 (1993).
HSSP; P07130; IDLC.
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MCBL_TaxID=1428;
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    1118 TEQUWIDMSETEGUFNIESVELVLREE 1144
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GO; GO:000592; P:defense response; IEA.
InterPro: IPR001178; Endotoxin.
InterPro: IPR005639; endotoxin.C.
InterPro: IPR005639; endotoxin.N.
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Pfam; PP003945; endotoxin.C; I.
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Delta-endotoxin (Fragment).
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STRAIN-HD-9;
Mat lsa M.N., Abdullah M.A.F., Mahadi N.M.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, A7963025; AAK51084.1; -.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:00592; P:défense response; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.C.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI _TaxID=1436;.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Delta-endotoxin CrylBa2.
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                                                                                                                                                                             Gaps
                                                                                                   DB 2; Length 1228;
                                                                                                                                Indels 151;
InterPro; IPR008539; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00855; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
SEQUENCE 1228 AA; 139621 MM; 3DA2A4DBF59C95C3
                                                                                                   Ouery Match
42.1%; Score 2545.5; DB 2;
Best Local Similarity 43.8%; Pred. No. 1.6e-136;
Matches 558; Conservative 183; Mismatches 381;
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162 NAMPLFAIRNQEVPLLAVYAQAANLHLLLLADASLFGSEFGLTSQBIQRYYERQVERTRD 221 241 YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPWYDTRTYFIETTAQ 300 222 YSDYCVEWYNTGLANSLRGTNAASWVRYNQFRRDLTLGVLDLVALFPSYDTRTYFINTSAQ 281	301 LTREVYTDPIVFNRETSGGFCRRMSLNSDISFSEVESAVIRSPHLFDILSBIEFYTTRAG 360 282 LTREVYTDAIGATGVNMASMNWYNNNAPSFSAIEAAAIRSPHLLDFLEQLTIFSAS 337	361 LPLANTEYLEYWGHSIKYKNTNASSALBRNYGTITSNKIKYDLANKDIFQVR 414 : :: : : :	415 SLGADLANYYAQVYGVPYASFTLLDKATGGGSVGGPTYSKPHTTMQVCTQNYNTIDBI 472	473 PPENEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKIT 530	531 QIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYAST 590	591 THEALFUTISGTRIYSINVNKTMAKGDDLIFNTFDLATIGTAFTFSNYSDSLTVGADSFA 650 :	651 SGGEVYVDKFELIPVNATFRAEEDLDVAKKAVNGLFTSKKD-ALOTSVTDYQVNQAANLV 709 	710 BCLSDELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRIN750	751 -GENGWTGSTGIEVARGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKL 809	910 KGFIGSSQDLEIKLIBHRANQIVKNVPDNILPDVLPVNSCGCIDRCSEQQYVDANL 865	866 ALENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEG 924	925 PLSGETLERACCOGOGOMODKWARKRGASEKAYYAAKQAIDRLFADYQDOKLNSGVEMSDM 984	985 IAAQNIVQSIPYVYNDALPEIPGRNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSD 1044 	1045 WNATSDVNVQQLSDTSVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDG 1104		NICDDIGGLADCTSTIAN OF 1251 CONTINUED OF 15 CONTINUED OF	1155 FNIESVELVLEER 1167 :: : 1216 FIVDSVELLLMEE 1228
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Db 856 DLDCSCRDGEKCAHHSHHFSLDIDVGCTDLHENLGVWVVFKIKTQEGHARLGNLEFIEEK 915 Qy 925 PLSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVENSDM 984	OY 985 LAAQNIVQSIPYVYNDALPEIPGANYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSD 1044	OY 1045 WNATSDVAVQQLSDTSVLVIPNWNSQVSQOFTVQPNYRYVLRVTARKEGVGDGYVIIRDG 1104	Oy 1105 ANQTETLTP 1113	Oy 1114NICDDDTGVLSADQTSYITKTVBFTPSTEQVWIDMSETBGV 1154	Oy 1155 FNIESVELVLEER 1167	RESULT 4 O93NMS	ID Q93NMS PRELIMINARY; PRT; 1228 AA. AC Q93NMS CONTROL OF CONTROL			RA Zhang J., Song F., Huang D.; RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. DR EMBL, APS68257, AAK63251.1; DR GO; GO:0015070; F:toxin activity; IRA.			SEQUENCE 1228 AA; Query Match Best Local Similarity	MSPNNQNEYELLDASSSTSVSDNSVRYPLANDQTTTLQNNNYKDYLRMSEGENPELFGNP 6	MIMKQVED	OY 121 LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180	181 AKIPSFAISGOEVPLLSVYAQAANLHLLLRDASIFGAEMGFTPGBISTFYD

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1033 NGDFNNGLSCWNVKGHVDVQQSHHRSDLVIPEWEAEVSQAVRVCPGRGYILRVTAYKEGY 1092
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Delta endotoxin.
Bacillus thuringiensis.
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus
NCBI_TAXID=1428;
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SEQUENCE FROM N.A.
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40.3%; Score 2433; DB 2; Length 1231;
Best Local Similarity 41.8%; Pred. No. 4.3e-130;
Matches 534; Conservative 205; Mismatches 380; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Island I.A., Isakov Y.B., Rymar' S.E., Yarovoi S.V.;

Cloning of a novel Bacillus thuringiensis crylBil gene for insecticidal crystal protein.", consistent of Aug. 2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AX138457; AAM93496.1; -...

GO; GO:0006952; P:defense response; IEA.

R GO; GO:0006952; P:defense response; IEA.

InterPro; IPR00549; endotoxin.C.

R InterPro; IPR005639; endotoxin.R.

InterPro; IPR008639; endotoxin.R.

InterPro; IPR008639; endotoxin.R.

R InterPro; IPR008539; endotoxin.C.

R Pfam; PP003944; endotoxin.C; 1.

R Pfam; PP03945; endotoxin.C; 1.

R Pfam; PP03945; endotoxin.C; 1.
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1231 AA; 139765 MW; C9F2848A9297EA00 CRC64;
                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                   1231 AA
                                                                                                                                                                   (TrEMBLrel. 22, C
(TrEMBLrel. 22, I
(TrEMBLrel. 25, I
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Bacillus thuringiensis
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SVPADYASAYEEKAYTDGRRDNPCBSNRGYGDYTPL.PAGYVTKELEYFPETDKVWIBIGE 1138
                                                                                                                        EMSDMLAAQNLVQSIPYVYNDALPBIPGMYTSPTBLTNRLQQAWNLYDLRNAIPNGDPR 1039
                                                              NGLSDWHATSDVHV-QQLSDTSVLVIPHWNSQVSQQPTVQPHYRYVTRVTARKEGVGDGY
                                                                                                                                                                                                                                                                                                                               VTIHBIENNIDELKPSNCVEBEVYPNNTVTCNDYTATQEEYEGTYTSRNRGYDGAYESNS
  -SHHPSLDIDVGCTDLNBBLGVWVIPKIKTQDGHARLGNLB
                                          LVEEGPLSGETLERAQQQEQQWQDXWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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SPRCTES=B.-thuringlensis, STRAIN=T84A1;
SPRCTES=B.-thuringlensis, Hatanaka C., Funatsu G., Hayashi K.;
Nagamatsu Y., Itai Y., Hatanaka C., Funatsu G., Hayashi K.;
"A Toxic Fragment from the Entomocidal Crystal Protein of Bacillus
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

A Zhong W.F., Cat P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
Zhong W.F., Cat P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
Zhong W.F., Cat P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
Zherial gene cloned from Bacillus thuringiensis serovar sott
E Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB026261; BAA77213.1; -.

R PIR, A22798; A22798.

R HSSP; P02965; 1CIY.

R GO; GO:0006952; Picefense response; IEA.

R GO; GO:0006952; Picefense response; IEA.

R InterPro; IPR001178; Endotoxin.

R InterPro; IPR00538; endotoxin.C.
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SPECIES-B.thuringiensis; STRAIN=T84A1;
Ogo M., Yamada S., Kobayashi Y., Shibata J., Nagamatsu Y.;
"Nuclectide Sequence of the Lepidoptera-toxic Protein Genethuringiensis subsp. dendrolimus T84A1.";
J. Fac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis, and
Bacillus thuringiensis (subsp. sotto).
Bacteria; Firmitutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428, 29340;
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Nagamatsu Y.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                           VIIRDGANQTETLTFN-----ICDDDTGV----
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Brie4A1 crystal protein (Crystal protein Crylh).
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TEGTFIVDSVELLLMEE 1155
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                                                                                                                                                                                                                                                                                                                                                                                                                   64 IWGIPGPSQ----WDAPLVQIEQLINQRIEEPARNQAISRLEGGLSNLYQIYAESFREWEA 119
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                     167;
                                                                                                                                                                                                                               2; Length 1155;
                                                                                                                                                                                                                          Query Match 34.0%; Score 2056.5; DB 2; Length Best Local Similarity 39.2%; Pred. No. 1.2e-108; Matches 477; Conservative 184; Mismatches 389; Indels
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:006952; P:defense response; IEA.
InterPro; IPR00173; Bndocoxin.
InterPro; IPR0015639; endotoxin.C.
InterPro; IPR005639; endotoxin.N.
InterPro; IPR009599; Gal.bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin; C; 1.
Pfam; PP03445; endotoxin.C; 1.
SEQUENCE 1155 AA; 130557 MW; 5D69E3E2P527749D CRC64;
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                                          OKLINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSPTELTNRLQQAWNLYDLRNA
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33.9%; Score 2048; DB 2; Length 1176;
Best Local Similarity 39.3%; Pred. No. 3.8e-108;
Matches 480; Conservative 174; Mismatches 414; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yao J., Zhang J., Song F., Chen Z., Li C., Huang D.;
"A novel crylaa gene from Bt atrain 1y30.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF344211; AAP80146.1; -
SEQUENCE 1176 AA; 133169 WW; 725C14EA9408869B CRC64;
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Last sequence update)
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1428;
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InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1180 AA; 133489 MW; 1199E4A6DIDCE62D CRC64;
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                                                                    GSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPPENB--PLSRGYSHRLSHITSYSFSKNAS
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CRYIA(A).
Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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33.8%; Score 2045; DB 2;
Best Local Similarity 39.3%; Pred. No. 5.7e-108;
Matches 479; Conservative 174; Mismatches 415;
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                                  SGSFRIVGFTIPPNFSNGSSVFILSAHVFNSGNBVYIDRIEFVPABVTFBABYDLBRAQK 621
                                                                                                                                                LLQDTGPNRING--ENGWTGSTGIEVAEGDVLFKDRSLRLTSARBIDTETYPTYLYQQID 797
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                                                                               PNTFDLATIGTAFTFSNYSDSLTVGADSFASGGBVYVDKFELIPVNATFEABBDLDVAKK
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Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ
REMEJ, AFI154676; AAD55382.1; --
HSSP; P02965; ICIY.
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GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0006952; P:defense response; IEA.
InterPro; IPR001503; endotoxin C.
InterPro; IPR001503; endotoxin N.
InterPro; IPR001503; endotoxin N.
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IGETEGTPIVDSVELLLMEE 1176
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973 OXINSGVEMSDMIAAQNIVQSIPYVYNDALPEIPGMNYTSFTELTNRLOQAWNLYDLRNA 1032
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                                                                                                                                                                                                                                                                                                                            VLDLVALPPNYDTRTYPIBTTAQLTREVYTDPIVPNRETS-GGFCRRWSLNSDISFSBVE 336
                                                                                                                                                                                                                                                                                                                                                                                                        NYGTITSNXIKYYDLANXDIPQVRS-----LGADLANYYAQVYGVPYASPTLLDRNT 442
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                                                                                                                                                                                                                                                                                                                                            SAVIRSPHIFDILSEIBFYT-TRAGLPLNNTEYLBYWYGHSIK----YKNTNASSALER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAGNAAPPVL--VSLTGLGIPRTLSSPLYRRIILGSGPNNQBLFVLDGTEFSFASLTTNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLQDTGFNRING--ENGWTGSTGIEVAEGDVLPKDRSLRLTSAREIDTETYPTYLYQQID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 ATLGNIELVEEGPISGETLERAQQQEQQWQDKWARKGASEKAYYAAKQAIDRLFADYQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 NPEL-----PGNPBT-PISSTVQTG---IGI---VGQVLGALGVPPAGQIASFYSF
                                                                                                                 NPNINECIPYNCLSNPEVEVLGGGRI BYGYTPIDISLSLTQPLLSBFVPGAGFVLGLVDI
                                                                                                                                                                                                                                                                  AEWGPTPGBISTPYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854 RCSEQQYVDANLALENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGY
                                                                                                                                                                                                       NRNDTRARSVVVTQY1ALELDPVAKIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIFG
                           Length 1176;
                                                          Indels
1176 AA; 133010 MW; FCEE069D0B81D8C4 CRC64;
                             33.7%; Score 2034; DB 2;
llarity 39.2%; Pred. No. 2.4e-107;
Conservative 173; Mismatches 417;
                                            Local Similarity
les 478; Conserv
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NGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGY 1098
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                     S-IRSPHIMDILNSITIYT----DAHRGEY--YWSGHQIMASPVGFSGPEFTFPL---Y 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLKPYTRYKLKGFIGSSODLBIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQ 859
                                                                                                                                                                                                                                                                       920 LVEEGPLSGETLERAQQQEQQWQDXWARKRGASEKAYYAAKQAIDRLFADYQDQKLMSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1123 -LSADQTS-----YITKTVEFTPSTEQVWIDMSE
                                                                                                                                                                                                                                                   SGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFN
                                                                                                                                                                                                                                                                                                                                     SPRINGETIPENESIGSSVETISAHVENSGNEVYIDRIBEVPAEVTEBARYDLERAQKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPPNFRGINRQLDRGWRGSTDITIQGGDDVFKENYVILLGTFD---ECYPTYLYQKIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         980 EMSDMLAAQNLVQSIPYVYNDALPEIPGMYYTSFTELTNRLQQAWNLYDLRNAIPNGDFR
                                                                                                                           447 VGGFTYSKPHTTMQVCTQNYNTIDEIPPENE--PLSRGYSHRLSHITSY--SPSKNASSP
                                                                                                                                                                                                          NGLFTSKKD-ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKBAKRLVQARNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               860 YVDANLALENNGENGNMSSDSHAPSPHIDTGEIDLMENTGIWVVFKIPTTNGYATLGNLE
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                                                             GTITSNKIKYYDLANKDIPQVRSLGADLANYYAQVY--GVPYASPTLLDKNT----GSGS
                                                                                             GIMGNAAPQQRIVAQLGQGVYRTLSSTL---YRRPFNIGINNQQLSVLDGTEPAYGTSSN
                                                                                                                                               LPSAVYRKSGTV-----DSLDEIPPQUNUVPPRQGFSHRLSHVSMFRSGFSNSSVSI
                                                                                                                                                                                         503 ARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTS
                                                                                                                                                                                                                                                                                                                      TPDLATIGTAFTPSNYSDSLTVGADSFASGGEVYVDKFELIPVNATFEAEBDLDVAKKAV
AVIRSPHLFDILSBIBFYTTRAGLPLANNTBYLEYWVGHSIK----YKNTNASSALERNY
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Yu J., Tan L., Wu D., Pang Y.;

"Molecular characterization of a silent gene encoding a 130-kilodalton crystal proctein from Bacillus thuringiensis subsp. israelensis.";

T crystal procts from Bacillus thuringiensis subsp. israelensis.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

BYR1, A29125; A29125.

R GO; GO:0015970; F:toxin activity; IEA.

R GO; GO:0015970; F:toxin activity; IEA.

R InterPro; IPR00138; endotoxin. C.

R InterPro; IPR005639; endotoxin. C.

R InterPro; IPR005639; endotoxin. 1.

R Pfam; PP03944; endotoxin. 1.

R Pfam; PP03945; endotoxin. 2. 1.

R Pfam; PP03945; endotoxin. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEWGFTPGEISTFYDROVTRTAOYSDYCVKWYNTGLDKLKGTNAASWLKYHOFRREMTLL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 IVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRNDTRARSVVVTQYIALELDFVAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : | : |: || : || || || DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYRVPLLSVYVQAVNLHLSVLRDVLVFG 179
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   IPNGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRVVLRVTARK
                                                                                                                                DTGVLSADQTS-----YITKTVEFTPSTEQVWID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
33.6%; Score 2032.5; DB 2; Length
Best Local Similarity 38.9%; Pred. No. 2.9e-107;
Matches 473; Conservative 185; Mismatches 392; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillus thuringiensis (subsp. israelensis).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI _TaxID=1430;
                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                          PRT; 1155 AA
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IGBTEGTFIVDSVELLIMER 1176
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WNATSDVNV-QQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRD 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                923 HAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIPTAFSLYDARNVIKNGDFNNGLSC
                                                        692 ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKRAKRLVQARNLLQDTGFNRIN-
                                                                                                                                                                                          -GENGWIGSTGIBVARGDVLPKDRSLRLTSARRIDTBTTYPTYLYQQIDESLLKPYTRYKL
                                                                                                                                                                                                              OPDRGWRGSTDITIQGGDDVFKENYVTLPGTFD---ECYPTYLYQKIDESKLKAYTRYEL
                                                                                                                                                                                                                                                                                          PLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAI DRLFADYQDQKLNSGVEMSDM
508 INSPITQRYRLRFRYASSRDARITVAIGGQIRVDWTLBKTMBIGBSLTSRTFSYTNPSNP
                                                                                                                                                                                                                                                                  KGPIGSSODLEIKLIRHRANQIVKNVPDN----LLPDVLPVNSCGGIDRCSEQQYVDANL
                                                                                                                                                                                                                                                                                                                                                866 ALE-INGENGNMSSDSHAFSPHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVBEG
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                                      PTPSNYSDSLTVGADSPASGGEVYVDKPELIPVNATFEAREDLDVAKKAVNGLFTSKKD-
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SEQUENCE FROM N.À.

SITAIN-B-Pr-86;

LIC., Zhang J., Li G., Huang D.;

A LiC., Zhang J., Li G., Huang D.;

Li Submitted (JUL-2000) to the EMEL/GenBank/DDBJ databases.

EMELY, AF286833 AAO13756.1;

RO; GO:0006952; P:defense response; IEA.

RO; GO:0006952; P:defense response; IEA.

RINEEPRO; IPR00178; Endotcoxin.

RINEEPRO; IPR005639; endotcoxin.

RINEEPRO; IPR008539; endotcoxin.

RINEEPRO; IPR008549; endotcoxin.

RINEEPRO; PR008559; endotcoxin.

R Pfam; PF00555; endotcoxin.

R Pfam; PF03944; endotoxin.C; 1.
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Last annotation update)
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                                                                                                                                              Barboza-Corona J.E., Lopez-Meza J.E., Ibarra J.E.;
"Cloning and expression of the crylads gene of Bacillus thuringiensis
and the comparative toxicity of its gene product.";
World J. Microbiol. Biotechnol. 14:437-441(1998).
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                                                                                                                                                                                                                                                            Thera J.E., Barboza-Corona J.E.;

Ibara J.E., Barboza-Corona J.E.;

Ibara J.E., Barboza-Corona J.E.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: 194323; AJ00732.1; -.

PIR; A37829; A37829.

R GO; GO:0015070; F:toxin activity; IEA.

GO; GO:0006952; P:defense response; IEA.

InterPro; IPR001178; Endotoxin. C.

InterPro; IPR005639; endotoxin. C.

InterPro; IPR005639; endotoxin. C.

R InterPro; IPR008979; Gal bind Tike.

Pfam; PP00395; endotoxin. J.

R Pfam; PP003945; endotoxin. N; 1.

Pfam; PP03944; endotoxin. N; 1.

R Pfam; PP03945; endotoxin. N; 1.
                                  Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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                                                                                                              PROM N.A.
                                                                                            [1] SEQUENCE FROM N.?
STRAIN=LBIT-147;
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| STRAIN=A-F;
| A Yu J., Pang Y., Li J.;
| T. (Cloning and sequence analysis of the crylCa6 gene from Baci thuringiensis, strain A2-F.";
| L. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
| R. EMBL, AF21547; AAF37224.1;
| R. EMBL, AF21547; AAF37224.1;
| R. EMBL, AF21567; P. Toxin activity; IRA.
| R. GO; GO:0015070; P. Froxin activity; IRA.
| R. GO; GO:0015070; P. Froxin activity; IRA.
| R. GO; GO:0015070; P. Froxin activity; IRA.
| InterPro: IPR00551; endotoxin C.
| R. InterPro: IPR00555; endotoxin N.
| R. Fam; PF00555; endotoxin N.
| R. Fam; PF00545; endotoxin N; 1.
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
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Last annotation update)
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                                                                                                                                                        Gaps
                                                                                                                                                 Indels 148;
                                                                                             Length 1169;
   Pfam; PF03945; endotoxin N; 1.
SEQUENCE 1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
                                                                                      Query Match
33.1%; Score 2003; DB 2; I
Best Local Similarity 39.3%; Pred. No. 1.4e-105;
Matches 460; Conservative 173; Mismatches 389;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus NCBL_TaxID=1428;

SEQUENCE FROM N.A.

Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases

INFORMATION." STRAIN=BTS00349A;

2

Lambert

SEQUENCE FROM N.A. STRAIN=B-Pr-88;

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987 AQNLVQSIPYVYNDALPBIPGAMYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWN 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                 NNLTIFTDWFSVGRN----FYWGGHRVISSLIGGGNITSPIYGREANQEPPRSFTFNGP 359
                IFQVRSIGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTI 469
                                 360 VP--RTLSNPTLRILQOPWPAPPFNLRGVBGVEPSTPTNSFTYRGRGTV-----DSL 409
                                                 DEIPPENE--PLSRGYSKRLSHITSYSPSKNASSPARYGNLPVFAWTKRSADVTNTVYSD 527
                                                            |:|||: | |||||| | ||: :||
410 TELPPEDNSVPPREGYSHRLCHAT---FVQRSGTPFLTTGV-VFSWTHRSATLTWTIDPR 465
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                                                                                                                     ASTTNIRLEVT-----ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSD
                                                                                                                                 ENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVERGPL
                                                                                                                                                        SLTV-----GADSPASGGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSKKO-AL
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A Li C., Zhang J., Huang D., Li G.;

"A crystal endotoxin from Bacillus thuringiensis strain B-P:
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; Z2211; CA880235.1; -.
EMBL; AF336114; AA013295.1; -.
EMBL; AF33619; S12649.
R FRB; S32649; S12649.
R GO; GO:0015070; P:toxin activity; IRA.
GO; GO:0015070; P:toxin activity; IRA.
R GO; GO:005952; P:defense response; IBA.
InterPro; IPR001178; Endotoxin.
R InterPro; IPR005639; endotoxin.
R InterPro; IPR005639; endotoxin.
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Q45749 PRELIMINARY; PRT; 1174 AA. Q45749; 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update) Crystal protein (Crystal delta-endotoxin). CRYIFB.

Bacillus thuringiensis.

045749 1D 049 AC 044 DT 011 DT 010 DE CT 08

RESULT 15

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993 SIPYVYNDALPEIPGMNYISFIELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVN 1052
                                                                                                                                                                                                                                                     TF----- 1113
                                                                                                                                                                                                                                                                    1050 KPSNCVEEGYPNNTVTCNEYTMNQGVGECTDACNVRNRGYEDAYGHNPSTPVHYTTPYEE 1109
STGIEVARGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQ 817
                                                                     DLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLALENNGEN 873
                                                                                                     DLEIYLIRYNSKHEIVAVVPGTGSLWPLSVENQIGPCGEPURCA--PHLEWNPDLHCSCRD 809
                                                                                                                          GNMS-SDSHAPSPHIDTGEIDLINENTGIWVVPKIPTTNGYATLGNLELVEEGPLSGETLE 932
                                                                                                                                   933 RAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLMSGVEMSDMLAAQNLVQ 992
                                                                                                                                                                  930 RIREAYLPELSVIPGVAAAIFEELEGRIFTAYSLYDARNVIKOGNFUNGLLCWNVKGHVD 989
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1170 LLMEE 1174
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409 DIFQVRSLGADLANYYAQVYGVPYASFTLLDXNTGSGSVGGPTYSKPHTTMQVCTQNYNT 468
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1 MSPNNQNEYEILDASSSTSV......MSETEGVFNIESVELVLEEE 1167
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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parasporal crystal	parasporal crystal	parasporal crystal	cryV465 protein -	insecticidal prote	parasporal crystal	insecticidal prote	parasporal crystal	parasporal crystal	-	parasporal crystal	-	parasporal crystal	parasporal crystal	protoxin - Bacillu	hypothetical prote
USBSBI	139870	A26858	I40590	I39815	525383	I39814	A22798	S04181	139811	S10228	A27323	B29838	JH0261	JC7140	B42459
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136	1180	1180	719	719	719	719	934	823	652	629	652	934	649	655	380
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ALIGNMENTS

rotein .; Авап

paragporal crystal protein cry9Cal [validated] - Bacillus thuringiensis

N;Alternate names: parasporal crystal protein cryIH
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Batcession: A59350; 849247
R;Lambert, B.; Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
R;Lambert, B. Buysse, L.; Decock, C.; Jansens, S.; Piens, C.; Saey, B.; Seurinck, J.; V
Appl. Environ. Microbiol. 62, 80-86, 1996
A;Title: A Bacillus thuringiensis insecticidal crystal protein with a high activity agai
A;Reference number: A59350
A;Molecule type: DMA
A;Residues: 1-1157 < LLMA
A;Residues: 1-1157 < LLMA
A;Residues: 1-1157 < LLMA
A;Residues: 1-1157 CLMA
C;Comment: This parasporal crystal protein, active against corn borer and other insects, C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein

Query Match

51.7%; Score 3123; DB 1; Length 1157;

| IPGMAYTSFTELTNRLQQAMNLYDLRNA|PNGDFRNGLSDWANTSDVNVQQLSDTSVLVI | 1064

1005

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14; 1004 119 461 180 239 359 WGLCRRWGTWPYNTPSELENAFIRPPHLFDRLMSLTISSNR- 359 416 413 474 532 518 592 578 646 638 706 698 KGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIBTTA 299 LWDAVKEARCLVQARNILQDTGFNRING--ENGWTGSTGIEVA 764 758 824 814 884 874 FHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLERAQQQEQQHQDK 944 SYINTGDLAASVDQGIWVVLKVRTTDGYATLGNLELVBVGPLSGBSLERBQRDNAKMNAB 934 9 |||||| :|||:||:||| :|||| || || || ||:||| HHHKVHLVRAVPDNLVSDTYSDGSCSGINRCDBQPQWQLDAEHHPWDCCRAAQTHBPS KYKNTNASSALERNYGTITSNKIKY---YDLANKDIPOVRSL RRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IBST ISYSPSKN-ASSPARYGNLPVFAWIHRSADVINTVYSDKITQI |||||| ||:||:|| |GFTGGGILRRTINGTFGTLRVIVNSPLTQQYRLRVRFASTGN MARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNIVQSIPYVYNDALPE SGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIBFYTTRA SPTL--LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDEIPP VNATFEAEEDLDVAKKAVNGLFTSKKODALQTSVTDYQVNQAA RHRANGIVKNVPDNILLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAFS SVSDNSVRYPLANDQTTTTLQNMVYKDYLRMSBGENPBLFGNP ILOGI GDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDP SVYAQAANLHLLLLRDASI PGABWGPTPGBISTPYDRQVTRTA GFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN KINNKGDDLIFNIF---DLATIG---TAFTFSNYSDSLTVGA Gape 42; Indels / Pred. No. 4.4e-173; 195; Mismatches 327; 765 825 815 885 945 759 875 935 8 8 음 & ď ठे g ð 셤

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parasporal crystal protein cryBal - Bacillus thuringiensis subsp. thuringiensis parasporal crystal protein cryAt Balternate names: parasporal crystal protein cryAt C.Species: Bacillus thuringiensis subsp. thuringiensis C.Species: Bacillus thuringiensis subsp. thuringiensis C.Species: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 01-Dec-2000 C.Accession: S00873
R.Brizzard, B.L.; Whiteley, H.R.
Nucleic Acids Res. 16, 2723-2724, 1988
A.Title: Nucleotide sequence of an additional crystal protein gene cloned from Bacillus A.Reference number: S00873; MUID:88203216; PMID:3362680
A.Accession: S00873
A.Molecule type: DNA
A.Residues: 1-1228 <BRI:X06711; NID:940264; PIDN:CAA29898.1; PID:9580949
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43.8%; Pred. No. 1.3e-139;
ive 183; Mismatches 381;
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Keywords: delta-endotoxin
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A;Start codon: TTG
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N;Alternate names: delta-endotoxin-related protein; parasporal crystal protein cryX
C;Species: Bacillus thuringiensis
C;Date: 07-0ct-1994 #sequence_revision 01-Dec-1995 #text_change 01-Dec-2000
C;Accession: S39536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTRARSVVVTQYIALELDFVAKIPSFAISGQ-----EVPLLSVYAQAANLHLLLLLRDASI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLLVLDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGP----CRRWSLNSDI 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFSEVESAVIRSPHLFDILSEIEFTTTRAGLPLNNTEYLEYWVGHSI--KYKNTNASSAL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVOCFTYSKPHTTMQVCTQNYNTIDEIP--PENEPLSRGYSHELSHITSYSP----SK 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYKDYLKMSEGDYIDSYINPGNV--RTGLQTGIDIVAVVVGALGGPVGGILTGFLSTLPG 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 NYKOYLAMSEGRNPELFGNPETPISSSTVQTGIGIUGQVIGALGVPFAGQIASFYSFIUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVRA-NLVLQRPEILHALFVSSMPSFG-SGPGSQRFQAQLLVVYAQAANLHLLLLADAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERNYGTITSNKIKYYDLANKDIFQVRS---LGADLANYYAQVYGVPYASFTLLDKNTGSG
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                                                                                       PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVI IRDGANQTBTLTPNI CDDDTGVLS
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                                                                                                                                                                                                                                                                                                            45.5%; Score 2750.5; DB 2; Length llarity 48.7%; Pred. No. 1.9e-151; Conservative 197; Mismatches 341; Indels
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1154 <SHE>
A;Cross-references: RMBL:X75019
C;Superfamily: parasporal crystal pr
C;Keywords: delea-endotoxin
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Best Local S:
Matches 562
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요 8	DPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGELMPRGR-DQWEIFLEHVEQ	ον 1114
중 옵	121 LIDOLIUSVYKIALALOLIOOLOOPIONAAN KANALAKKUTIRAKSVYVYTOILALELEV 180 	1156
à à	181 AKIPSFAISGGEVPLLSVYAQAANLHLLLERDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240 	Oy 1155 FNIES :: Db 1216 FIVDS
8 &	YSDYCVKAYNTGLDKLKGTNAASWLKYHQPRREATLLVLDLVALPPNYDTRTYPI BTTAQ 	RESULT 5 A48944 parasporal crystal
ò a	301 LTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIRFYTTRAG 360 ::	N;Alternate names: C;Species: Bacillus C;Date: 19-Dec-1993 C;Accession: A48944
රු සි	LPLINNTEYLEYWYGHSIKYKNTNASSALERNYGTITSNKIKYYDLANXDIFQVR : :: :: :: :: SRWSNTRHMITWRGHTIQSRPIGGGLMTSTHGATNTSINPYTLRFASRDYYRTE	R;Lambert, B.; Hoft Appl. Environ. Micr A;Title: Novel Baci A;Reference number:
ት 8	415 SLGADLANYYAQVYGVPYASFTLLDKAYTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBI 472	A;Contente: BTS137J A;Accession: A48944 A;Status: prelimina A;Molecule type: DN
ት ብ	473 PPBNEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKIT 530	A; Residues: 1-1138 A; Cross-references: A; Note: sequence ex C; Superfamily: para
දි සි	531 QIPVVRAHTLVSGTIVVKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYAST 590 :	C; Keywords: delta-e Query Match Best Local Simila Matches 514. Co
රු දු	591 TNLRLPVTISGTRIYSINVNKTMAKGDDLTFNTPDLATIGTAPTPSNYSDSLTVGADSFA 650 : : : : : :	Matches 511;
<u>ያ</u>	651 SGGEVYVDKPELIPVNATFRAREDLDVAKKAVNGLFTSKKD-ALGTSVTDYQVNGAANLV 709 	. 19 j
8 9	710 BCLSDBLYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN750 :	
r B	751 -GENGWIGSTGIEVABGDVLPKDRSLRLJSAREIDTETYPTYLYQQIDBSLLKPYTRYKL 809 	Oy 181 AXIPS
s q	910 KGFIGSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGIDRCSEQQYVDANL 865 : :	241
è 8	866 ALENNGENG-NMSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEBG 924 :::	301
දු දු	925 PLSGETLERAQQEQQWQDKWARKRGASEKAYYAAKQAIDRLPADYQDQKLMSGVEMSDM 984	359
<i>∂</i> 8	985 LAAQNLVQSIPYVYNDALPEIPGRNYTSFTELTNRLQQARNLYDLRNAIPNGDFRNGLSD 1044 	339 416
රු සි	1045 WNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARYBGKGGGYVIIRDG 1104 - - - -	476
දී පිර	1105 ANQTETLTP 1113 	Qy 534 VVKAH

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fte, H.; Annys, K.; Jansens, S.; Soetaert, P.; Peferoen, M. crobiol. S8, 2536-2542, 1992.
cillus thuringiensis insecticidal crystal protein with a silent activit r: A48944; MUID:92384571; PMID:1514800
SFAISCOEVPILSVYAQAANIHLILEDASIFCAEWGFIPGEISTFYDRQVTRTAQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINNTE-YLEYWVGHSIKYKONTNASSALERNYGTITSNKIK--YYDLANYDIFQVRS 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHEIQPDLFYWSAHKVSFKKSEQSNLYTTGIYGKTSGYISSGAYSFHGNDIYRTLA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LANYYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPPE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VYTOPIVFNRETSGGFCRRWSLNSDI--SPSEVESAVIRSPHLFDILSBIBFYTTR 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRGYSHRISHITSYSPSKNASSPARYGN--LPVFAWTHRSADVTNTVYSDKITQIP 533
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parasporal crystal protein cryIIIC
; thuringiensis
| #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSTVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLHPSSTVSVWEMIMKQVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                         B: GB:M64478; NID:g142760; PIDN:AAA22351.1; PID:g142761
extracted from NCBI backbone (NCBIN:112092, NCBIP:112093)
rasporal crystal protein
endotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.7%; Score 2458.5; DB 2; Length 1138; larity 43.5%; Pred. No. 1.6e-134; Onservative 208; Mismatches 400; Indels 59;
                                                                                                   |||||:||||
|SVELLLMEE 1228
                                                                           SVELVLEER 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                    NA; protein
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nce extracted from NCBI backbone (NCBIN:92865, NCBI: parasporal crystal protein	Query Match Best Local Similarity 41.5%; Pred. No. 5.7e-119; Matches 501; Conservative 195; Mismatches 414; Indels 98; Gaps 24;	CY S NONEYELLDASSTSVSDNSVRYPLANDQTTTLQNANYKDYLRMSEGENPELFCNPETF1 64	Qy 65 SSSTVQTGIGIVGQVLGALGVP-FAGQIASFYSFIVGOLMPSSTVSVWE 112	QY 113 MIMKQVBDLIDQKITDSVRKTALAGLÇGLGDGLDVYQKSLKNMLENRNDTRARSVVVTQY 172 : : : :	OY 173 IA-LELDFVAKIPSFAISGOEVPLLSVYAQAANLHLLILRDASIFGAEMGF 222	OY 223 TPGEISTPYDROVTRTAQYSDYCVKMYNTGLDKLKGTNAASWLKYHOPRREMTLLVLD 280 :	Qy 281 IVALPENYDTRITYAQLTREVYIDPIVENRETSGGFGRRWSLMSD1SP 332	Qy 333 SEVESAVIRSPHLPDILSEIEPYTTRAGLPLN-NTEYLEYWVGHSIKYKNTNASSALERN 391 	Qy 392 YGTITSNKIKYYDLANKDIRQVRSLGADLANYYAQVYGVPYASFTLLDKNYGSG 445	
502 AVEMYKLDDPSTVVKGPGFTGGDLVKRGSTGYIGDIKATVNSPLSQKTRVRVRYATNVSG 594 RLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADS 594 RLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADS 595 QFNVYINDKITLQTKPQNTVBTIGEGKDLTYGSFGYIEYSTTIQFPDEHPKITLHLSD	Dy 649 FASGGEVYVOKFELLIVNATFEABEDDDVAKGAVNGLFTSKUDALOTSVTDYONQAANL 708 :: : :: :	CY 709 VECLSDELYPNEKRALWDAVKRAKRLVQARNILQDYGFNRINGENGWYGSTGIEVABG 766 : : : : :	OY 767 DYLFYDRSIRLTSARRIDTETYPTYLYQQIDESLLKDYTRYKLKGFIGSSQDLBIKLIRH 826 : : :	OY 827 RANGIVKNVPDNLLPDVLPVNSCOGIDRCSBOOYVDANLALENNGENGNMSSDSHAFSFH 886	QY 887 IDTGEIDIMENTGIWVPKIPTINGYATLGHLEHVEEGPLGGETLERAQQQEQQWQDKWA 946	CY 947 RKRGASEKAYYAAKQAIDRLFADYQDQKLAKGVEMSDMLAAQHLVQSIPYVYNDALPEIP 1006 : ::	QY 1007 GMNYTSFTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN 1066	Qy 1067 WNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLIFENICDDDTGVLSAD 1126 :: : : :	Qy 1127 QTSYITKTVEPTPSTEQVWIDMSETECVFNIESBE 1167 :	RESULT 6 S19306 parasporal crystal protein cry9hal - Bacillus thuringiensis parasporal crystal protein cry9hal - Bacillus thuringiensis parasporal crystal protein cry9hal - Bacillus thuringiensis glades and and seases delta-endotoxin; insecticidal crystal protein; parasporal crystal prof. Species: Bacillus thuringiensis C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000 G;Accession: S19306; A44847; S14602; S14837 R;Smulevitch, S.V.; Osterman, A.L.; Shevelev, A.B.; Kaluger, S.V.; Karasin, A.I.; Kadyro FEBS Lett. 293. 25-28, 1991 A;Artie: Nucleotide sequence of a novel delta-endotoxin gene cry1g of Bacillus thuringiensis and A;Reference number: S19306; WUID:92070568; PMID:1660003 A;Artie: Nucleotide sequence of a novel delta-endotoxin gene cry1g of Bacillus thuringiensis and A;Residues: 1-1156 <8MU A;Residues: 1-1156 <8MU A;Residues: 24-34 <8MU A;Reference number: A44847; MUID:9211329; PMID:1556556 A;Accession: Shoot of an insecticidal crystal protein from Bacillus thuringiensis I A;Reference number: A44847; MUID:92211329; PMID:1556556 A;Accession: A44847 A;Attle: Identification of an insecticidal crystal protein from Bacillus thuringiensis I A;Reference number: A44847; MUID:92211329; PMID:1556556 A;Accession: A44847 A;Attle: Identification of an insecticidal crystal protein from Bacillus thuringiensis I A;Residues: 1-1151 (GLE> A;Residues: EMBi.X58534; NID:948879; PIDN:CAA41425-1; PID:948880 A;Experimental source: isolate DSIR517

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993 SIPYVYNDALPRIPGMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVN 1052
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Baccession: S32645
R;Lambert, B.
submitted to the EMBL Data Library, April 1993
A;Rcession: S32645
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                                SCIIDSLDEIPPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSW-RAPWFSWTHRSATP
                                                                                                                                                        TONYNTIDEIPPENBPLS - - RGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADV
                                                                                                                       TWTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQR
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A;Cross-references: EMBL:222510; NID:9295861; PIDN:CAA80233.1; PID:9295862
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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parasporal crystal protein crylFal - Bacillus thuringiensis (strain aizawai)
N;Alternate names: parasporal crystal protein crylF
C;Species: Bacillus thuringiensis
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C;Accession: A42459 #sequence_revision 10-Jul-1992 #text_change 01-Dec-2000
C;Accession: A42459
A;Title: Isolation and characterization of a novel insecticidal crystal protein gene fro
A;Accession: A42459
A;Accession: A42459
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A;Cossion: A24
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                                                                                                                                                                                        NGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKBGVGDGYV 1099
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                                LVERGPLSGETLERAQQQEQOWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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Query Match 34.6%; Score 2093.5; DB 2; Length 1166; Best Local Similarity 39.7%; Pred. No. 2.7e-113; Matches 482; Conservative 172; Mismatches 392; Indels 167; Gaps 24;	59 NPETFISSSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLMPSSTVSWW 111	17 NPESBIFNAR-NSNFGLVSQVSSGLTRFLLBAAVPBAGFALGLFDIIMGALGVDQW 71	112 EMIMKQVEDLIDQKITDSVRKTALAGLGGLGDGLDVYQKSLKAWLENRNDTRARSVVVTQ 171	<u>jieolirģeitelernratailīcisssynlīv</u>	YIALELDFVAKU PSFALSGQEVPLLSVYAQAANIHLILLIRDASI FGABWGFTFGEISTFY	PRETIDDALVIGEPTEALRNEKVVNESVYTQAANEHESEERDAVYFGERMGETQANLEDEN	232 DROVIRTAQYSDYCVKWYNTGLBKLKGTNAASWLKTHGPRREWTLLVLLULVALFPNYDTR 291 192 TRILIGALIORYSDHCARWYNOGLINRIGGISH 18 - 1 -1 -1 -1 -1 -1 -1 -1 -1 -1	TYPE TRANSPORTED CONTRACTOR TO THE PROPERTY OF	TYPIPTQSQLTREIYTSPVVAGNINFGLSIANVLRAPHLMDFIDR	352 IEFYTTRAGLPLANTEYLEYWVGHSIKYKNTNASSALERNYGT 394	293 IVIYTNSVRSTPYWAGHEVISRRTGQGQGNEIRFPLYGVAANAEPPVTIRPTG 345	395 ITSNKIKYYDLANKDIFQVRSLGADLANYYAQVYGVFYASFTLLDKNTGSGSVGGFT-YS 453	346 FIDEORGMY-RARSRVVSFRSSGQDFSLVDAVGFLTIFS 383	454 KPHTIMOVCTONYNTIDBIPPENBPLSRGYSHRLSHITSYSFSKNASSPARYGNLFVF 511	384 AVSIYRNGFGFNTDTIDEIPIEGTDPFNGYSHRLCHVGFLASSPFISQYARAPIF 438	512 AWTHRSADVINTVYSDKITQIPVVKAHTLVSGTTVIKGPGFTCGNILKRISSGPLAYTSV 571	439 SWIHRSATLINITAPDVITQIPLVKAFNLASGATIVKSPGFTGGDILRRINVSSFGDMRV 498	572 SVKSPLSQRYRARIRYASITNLRLFVIISGTRIYSINVNKTWNKGDDLTFNTFDLATIGT 631	499 NITAPLSQRYRVRIRYASITDLQPYININGTIINIGNFSSTMDSGDDLQYGRFRVAGFTI 558	632 AFTFSNYSDSIJVGADSFASGGEVYVDKFELIPVNATFRAERDLDVAKKAVNGLFTSKKD 691	559 PPTFSDANSTFTIGAEGFSPNNEVYIDRIBFVÞAEVTFEAKYÐLBKAQKAVNALFTSSNQ 618	692 -ALQISVIDYQVNQAANLVECLSDELVPNEKRMLMDAVKEAKKLVQARNLLQDIGFNRIN 750	619 IGLKTDVTDYHIDKVSNLVECLSDERCLDEKRELSERVKHAKRLSDERNLLQDPNFRGIN 678	751GENGWIGSTGIEVAEGDVLFYDRSLRLTSAREIDTETYPTYLYQQIDESLLXPYTRYK 808 :	NYVILPGIFDGCYPTYLYQKIDBSKLKVYTRY	809 IKGPIGSSQDLBIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDAN 864	736 LRGYIEDSQDLEIYLIRYNAKHETVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWN 793	865 LALENNGENG-NMSSDSHAFSFHIDTGEIDLMENTGIWVVFKIPTTWGYATLGNLELVER 923	CSCRNGEKCAHHSHHFSLDIDVGCTDLNEDLA	924 GPLSGETLERAQQBQQWQDKWARKRGASBKAYYAAKQAIDRLFADYQDQKLASGVEMSD 983	854 KPLIČBALARVKRAEKKWRDKREKLELETNIVÝKRAKESVDALFVNSQYDQLQADTNIAM 913	984 MIAAQNIVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDERNAIPNGDFRNGLS 1043	914 IHAADKRVHSIRRAYLPRLSVIPGVNAAIFRRLEGRIFTAFSLYDARNVIRNGDFNNGLS 973
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'Accession: A26513
'Ocda, K.; Oshle, K.; Shimizu, M.; Nakamura, K.; Yamamoto, H.; Nakayama, I.; Ohkawa, H. ene 53, 113-119, 1987
'Title: Nucleotide sequence of the insecticidal protein gene of Bacillus thuringiensis; Reference number: A26513; MUID:87248103; PMID:3297927
-----VLSA 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 NPEL------FGNPET-FISSSTVQTG---IGI---VGQVLGALGVPFAGQIASFYSF 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                           arasporal crystal protein - Bacillus thuringiensis (strain aizawai);Species: Bacillus thuringiensis
;Bace: 11-Mar-1988 #sequence_revision 11-Mar-1988 #text_change 01-Dec-2000
                                                                                                                           4 NPNINECIPYNCLSNPBVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /;Accession: A26513
/;Status: preliminary
/;Molecule type: DNA
/;Residues: 1-1155 (ORD)
/;Constrainty: parasporal crystal protein
/;Superfamily: paraspotoxin
                                                                                                  ----ICDDDTG-
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1154 FIVESVELLIMEE 1166
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C.Superfamily: paraspozal crystal protein
C;Keywords: delta-endotoxin
C;Reywords: toxic peptide #status predicted
F;82-306/Region: toxic #status predicted
F;82-300/Region: toxic #status predicted
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NyAlternate names: delta-endotoxin-2; entomocidal protoxin; entomopathogenic crystal prof
C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Date: 28-Bcc11803 thuringiensis
C;Date: 28-Bcc11803 thuringiensis
C;Accession: A90025; A91560; A90555; S14555; A26461; A24172; A29043; JD0002
C;Accession: A90025
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes fro
A;Title: Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes fro
A;Reference number: A90025
A;Molecule type: mRNA
A;Residues: 1-1155 «KON>
A;Experimental source: subsp. kurstaki
R;Geiser, M.; Schweitzer, S.; Grimm, C.
Gene 48, 109-118, 1986
A;Title: The hypervariable region in the genes coding for entomopathogenic crystal prote
A;Recession: A91560; MUID:87163505; PMID:3557124
A;Recession: A9560
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                                                          RTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT1SGTR1YSINVNKTMNKGDDL
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A,Title: Structural and functional analysis of a cloned delta endotoxin of Bacillus thu A,Reference number: A26461; MUID:87054026; PMID:3023091 C.; Vandekerc gene product ans ŏ S-IRSPHIADILNSITIYT----DANKGEY--YWSCHQIMASPVGFSCPEFTFPL---Y 338 VIDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISPSEVBS 337 240 VLDIVSLPPNYDSRTYPIRTYSQLTREIYTNPVLRNFD--GSF--RGSAQG-----IEG 289 AVIRSPHLFDILSBIBFYTTRAGLPLANNTBYLBYWCHSIK----YKNTNASSALBRNY 392 GTITSNKIKYYDLANKDIFQVRSLGADLANYYAQVY--GVPYASFTLLDKNT----GSGS 446 LPSAVYRKSGTV-----DSLDBIPPQNNNVPPRQFSHRLSHVSMPRSGFSNSSVSI 447 64 IWGIFQPSQ----WDAFLVQIEQLINQRIEBFARNQAISRLEGLSNLYQIYAESFREWEA 119 VGGPTYSKPHTTMQVCTQNYNTIDEIPPENE--PLSRGYSHRLSHITSY--SFSKNASSP 502 98 IVGQLWPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLØGLGDGLDVYQKSLKNWLR 157 63 A;Residues: 1-730,'L',732-784,'R',786-1155 <HOP>
A;Cross-references: GB:X04698; NID:g40254; PIDN:CAA28405.1; PID:g40255
A;Experimental source: strain berliner 1715
c;Comment: This toxin is lethal to the larvae of lepidopterans and dipterans. 218 AEWGFTPGEISTFYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLL | | | : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 158 NRNDTRARSVVVTQYIALELDFVAKIPSPAISGQEVPLLSVYAQAANLHLLLRDASIFG 53 NPEL-----PGNPET-FISSSTVQTG---IGI---VGQVLGALGVPFAGQIASFYSF 4 NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLLSEFVPGAGFVLGLVDI A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1155 <CHA>
A;Residues: 1-1155 <CHA>
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
A;Cross-references: EMBL:X54939; NID:g40272; PIDN:CAA38701.1; PID:g40273
R;Hofte, H.; de Greve, H.; Seurinck, J.; Jansens, S.; Mahillon, J.; Ampe,
Eur. J. Biochem. 161, 273-280, 1986 A;Cross-references: GB:M15271; NID:g143123; PIDN:AAA22561.1; PID:g143124 A;Experimental source: subsp. kurstaki R;Wabiko, H.; Raymond, K.C.; Bulla Jr., L.A. DNA 5, 305-314, 1986 A;Title: Bacillus thuringlensis entomocidal protoxin gene sequence and A;Reference number: A90955; MUID:86300092; PMID:3743328
A;Accession: A90955 Query Match 34.1%; Score 2061.5; DB 2; Length 1155; Best Local Similarity 39.3%; Pred. No. 1.9e-111; Matches 478; Conservative 185; Mismatches 387; Indels 167;

change

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J. Mol. Biol. 208, 183-194, 1989
A.Title: Functional mapping of an entomocidal delta-endotoxin. Single amino acid of A; Reference number: S04994; MUID:89362455; PMID:2769751
A; Accession: S04994
A; Molecule type: DNA
A; Residues: 429-449, A*, 451-724 < HAW>
A; Residues: 429-449, A*, 451-724 < HAW>
A; Cross-references: EMBL:X16315
A; Cross-references: EMBL:X16315
C; Comment: This toxin is lethal to the larvae of lepidopterans and dipterans.
C; Superfamily: parasporal crystal protein
C; Keywords: delta-endotoxin
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                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                        Query Match 34.0%; Score 2052.5; DB 2; Best Local Similarity 39.4%; Pred. No. 6.3e-111; Matches 479; Conservative 183; Mismatches 388;
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A;Residues: 1-1155 «HAL»
A;Cross-references: EMBL:X13233; NID:g40277; PIDN:CAA31620.1; PID:g40278
A;Experimental source: strain aizawai IC1
R;Haider, M.Z.; Ellar, D.J.
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C;Species: Bacillus thuringiensis
C;Species: Bacillus thuringiensis
C;Species: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 01-Dec-2000
C;Accession: JC2219
R;Udayasuriyan, V; Nakamura, A.; Mori, H.; Masaki, H.; Uozumi, T.
Biosci. Blocken, S,8,810-815,1994
Birtile: Cloning of a new crylA(a) gene from Bacillus thuringiensis strain FU-2-7 and A;Reference number: JC2219; MUID:94289859; PMID:7764972
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---IRQPHLMDILNSITIYTDVHRG-----PNYWSGHQITASPVGFSGPRFAPLFG
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                                                                                                                                                                                                                                                                                                                                                                                                                       parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
parasporal crystal protein - Bacillus thuringiensis (strain aizawai IPL7)
NyAlternate names: 135K insecticidal protein
C;Species: Bacillus thuringiensis
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 01-Dec-2000
C;Accession: JT0241
A;Shimizu, M.; Oshie, K.; Nakamura, K.; Takada, Y.; Oeda, K.; Ohkawa, H.
Agritle: Cloning and expression in Bscherichia coli of the 135-kDa insecticidal protein
A;Reference number: JT0241
A;Reference number: JT0241
A;Residues: J-1176 cSHI>
A;Residues: 1-1176 cSHI>
A;Residues: 1-1176 cSHI>
C;Comment: The 135K protein has insecticidal activity against Plutella xylostella larvae
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
                                                                                                                                                              1098
                                                                                                                                                                            1122
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                                                                                                      EMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFR 1039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVGQLMPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 IWGIFGPSQ----WDAFLVQIBQLINQRIBEFARNQAISRLEGLSNLYQIYAESFREWRA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEWGPTPGBISTPYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLL 277
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                                                             | | : | | : | |: | |: VITHEIENNTDELKFSNCVEBEVYPNNTVTCNDYTATQEBYEGTYTSRNRGYDGAYESNS
                                                                                                                                                                                                                                                                                           : || | ::|||: | | | 1079 SVPADYASAYEEKAYTDGRRDNPCESNRGYGDYTPLPAGYVTKELBYPPETDKVWIEIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    920 LVEEGPLSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGV
                                                                                                                                                            NGLSDWNATSDVNV-QQLSDTSVLVI PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGY
                                                                                                                                                                                                                                                                              -LSADQTS-----YITKTVBFTPSTBQVWIDMSE
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                                                                                                                                                                                                                      VIIRDGANQTETLTFN-------ICDDDTGV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESLLKPYTRYKLKGFIGSSQDLEIKLIRHRANQIVKNVPDN----LLPDVLPVNSCGGID 853
                                                                                                                                                                                                                          64 IWGIFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEA 119
                                                                                                                                                                                                                                                                          SAVIRSPHLFDILSBIEFYT-TRAGLPLNNTEYLEYWVGHSIK----YKNTNASSALER 390
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A;Accession: JC2219
A;Molecule type: DNA
A;Residues: 1-1176 <UDA>
A;Residues: 1-1176 <UDA>
A;Cross-references: DDBJ:D17518; NID:g506190; PIDN:BAA04468.1; PID:g535781
C;Genetics:
A;Gene: cry1A(a)
C;Superfamily: parasporal crystal protein
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
                                                                                                                                                                                                                                                              NRNDTRARSVVVTQYIALELDFVAKIPSFAISGQEVPLLSVYAQAANLHLLLLRDASIFG
                                                                                                                                                                                                                                                                                                              ABWGPTPGBISTPYDRQVTRTAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NYGTITSNKIKYYDLANKDIFQVRS------LGADLANYYAQVYGVPYASFTLLDKNT
                                                                                                                                                              NPEL------FGNPET-PISSSTVQTG---IGI----VGQVLGALGVPPAGQIASPYSP
                                                                                                                                                                                     NPNINECI PYNCLSNPEVEVLGGERI ETGYTPIDI SLSLTQPLLSEFVPGAGFVLGLVDI
                                                                                                                                     Gaps
                                                                                                             Query Match
33.8%; Score 2045; DB 2; Length 1176;
Best Local Similarity 39.3%; Pred. No. 1.8e-110;
Matches 479; Conservative 174; Mismatches 415; Indels 152;
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Arasporal crystal protein cryAel - Bacillus thuringionsis (strain alesti)
C;Species: Bacillus thuringiensis
C;Accession: A41052
R;Lee, C.S.; Aronson, A.I.
J. Bacteriol. 173, 6615-6618, 1991
A;Reference number: A41052; MUID:92011442; PMID:1655719
A;Recession: A41052
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-1181 <LKB>
A;Cross-references GB:M65252; NID:g142874; PIDN:AAA22410.1; PID:g142875
C;Superfamily: parasporal crystal protein
C;Keywords: delta-endotoxin
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                                                                                            I PNGDPRNGLSDWNATSDVNV-QQLSDTSVLVI PNWNSQVSQQPTVQPNYRYVLRVTARK 1091
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OKLINSGVEMSDMLAAQNILVQSI PYVYNDALPEI PGMNYTSFTELTNRLQQAMNLYDLRNA
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                                                                                                                                              EGVGDGYVI IRDGANQTETLTPN------ICDD------
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Gaps

Indele 168; Length 1156

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979 VEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDF 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABWGFTPGEISTPYDROVTRIAQYSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLL 277
                                                                                                                                                                                                                                                                                     VLDLVALFPNYDTRTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVES 337
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                                                                                                                IVGQLMPSSTVSVWEMIMKQVEDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLE
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                                                                                                  53 NPEL-----FGNPET-FISSSTVQTG---IGI---VGQVLGALGVPFAGQIASPYSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>≕</u>
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C, Superfamily: parasporal crystal protein C, Keywords: delta-endotoxin
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A29125
paragoral crystal protein Bt2 - Bacillus thuringiensis subsp. kurstaki (strain HD-1)
C;Species: Bacillus thuringiensis subsp. kurstaki
C;Oate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 01-Dec-2000
C;Oate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 01-Dec-2000
C;Oate: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 01-Dec-2000
R;Fischhoff, D.A.; Bowdish, K.S.; Perlak, F.J.; Marrone, P.G.; McCormick, S.M.; Niederwe Bio/Technology 5, 807-813, 1987
A;Fitche: Insect tolerant transgenic tomato plants.
A;Reference number: A29125
A;Accession: A29125
A;Residues: 1-1156 cPIS>
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  GTMGNAAPQQRIVAQLGQGVYRTLS---STPYRNPFIIGINNQRLSVLDGTBPAYGSSSN 395
                                                                                                                                           SGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFN
                                                                                                                                                             NALFTSPNOIGLKTDVIDYHIDQVSNLVBCLSDBRPCLDBKRELSBKVKHAKRAKEDBERNIL
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                                                                                                                                                                                                                                                                                                                                                                                       VGGFTYSKPHTTMQVCTQNYNTIDBIPPB--NEPLSRGYSHRLSHITSY--SPSKNASSP
                                                                                      ARYGNLPVPAWTHRSADVTNTVYSDK1TQ1PVVKAHTLVSGTTV1KGPGPTGGN1LKRTS
                                                                                                    IR---APMPSWIHRSABPNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTS
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1160 IBIGETBGTFIVDSVELFLMEB 1181
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1098 YVIIRDGANQTETLIFN------ICDDDIGV------1122
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Search completed: June 21, 2004, 13:39:44 Job time: 34 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 21, 2004, 13:31:10; Search time 17 Seconds (without alignments) 3574.463 Million cell updates/sec

US-10-089-678-1 6044 1 MSPNNQNBYBILDASSSTSV......MSBTEGVFNIBSVELVLRBE 1167 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	045704	bacillus		bacillus	bacillue	bacillus		bacillus		bacillus	bacillus	bacillus	bacillus	bacillus	9415 bacillus	P05068 bacillus th																	
SUMMARIES	ΙD	C8AA BACUK		C8BA_BACUK	C9CA_BACTO	C9EA_BACTA	C9DA_BACTP	C1KA_BACTM	CLBB_BACTU	C1BA_BACTK	C1BC_BACTM	C1BE_BACTU	C7AA BACTU	C7AB_BACUA	C1BD_BACTZ	C7AB_BACUK	COAA_BACTF	C9AA_BACTG	C1FA_BACTA	C1GA_BACTU	CLJA_BACTU	CLUB_BACTU	CLAB BACTK	CLAB_BACTL	CLAA BACTK	C1EA_BACTX				1	C1DB BACTU	C1EB_BACTA	C1DA_BACTA	CLAC_BACTK
	Length DB			1169 1							1233 1		•	1138 1		1138 1	•					1170 1									1160 1		1165 1	1178 1
	Query Match L	66.3	61.8	52.2	51.7	46.7	44.9	44.9	42.2	42.1	41.2	40.7	40.7	40.7	40.5	40.4	36.9	v	S	4	d.	34.2	4	m	m	m	m	m	m	N	N	N	N	N
	Score	4007	3733.5	3152	3123	2825.5	2715	2714	2552	2547.5	2491	2462	2458.5	2458.5	2445	2439.5	2227.5	2191	2154.5	2093.5	2065.5	2065	2061.5	2044.5	2038	2024.5	2011.5	1999	1995	1991	1953.5	1946.5	1944	o
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C1CB_BACTG	C1AG_BACTU C1HB_BACTM CSAA_BACTP	C4BA BACTI C4AA BACTI C1ID BACTU	C11B_BACTE C11A_BACTK C11C_BACTU	CIAP_BACTU
1176 1	1176 1155 1109	1136 1180 719	719 1	911 1
31.8	31.1 31.1 30.9	20.9 29.4 9.4.0	28.7 28.5 26.9	24.2
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34	3 9 8 2 8 3 9	39 4 4 4 1 0	4 4 4 4 3 2	45

ALIGNMENTS

RESULT 1 CGAA_BACUK AC (45704; AC (4570
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1 MSPNNQNEYBILDASSTSVSDNSVRYPLANDQTTTLQNPAYKDYLRMSEGENPELFGNP 60

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RLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQ 1078
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                          ETFISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVBD 120
                                                                               LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV 180
MSPNNONBYBIIDATPSTSVSSDSNRYPPANBPTDALONMNYKOYLKMSGGENPELPGNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIPSFAVSGHEVILIAVYAQAVNIHILILIRDASIFGEEKGFTFGEISRFYNRQVQLTAE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                             Sato R., Takeuchi K., Ogiwara K., Minami M., Kaji Y., Suzuki N., Hori H., Asano S., Obba M., Iwahana H.; "Cloning, heterologous expression, and localization of a novel crystal protein gene from Bacillus thuringianiss serovar japonensis strain buibui toxic to scarabaeid insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the spore coat. MISCELLANDOUS; Toxic segment of the protein is located in the
                                                                                                                                                                       Pesticidial crystal protein cry8Ca (Insecticidal delta-endotoxin
CryVIIIC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxin; Sporulation.
SEQUENCE 1160 AA; 130425 MW; C16C3D912EBBB751 CRC64;
                                                                                                                                                                                                                                             Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        terminus. SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.8%; Score 3733.5; DB 1;
ilarity 64.2%; Pred. No. 4.4e-205;
Conservative 109; Mismatches 257;
                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last amnotation update)
Pesticidial crystal protein crysCa (Insecticida)
                                                                                                                                                                                                                               Bacillus thuringiensis (subsp. japonensis).
Bacteria, Firmicutes, Bacillales, Bacillaceae,
NCBI_TaxID=128936;
1139 PSTEQVWIDMSETECVFNIESVELVLREE 1167
| |:|:||::||| | ||||||::|
1129 PYTDQMWIEISETEGTFYIESVELIVDVE 1157
                                                                                                  PRT; 1160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, U04366; AAA21119.1; -.
PIR, I40589, I40589.
HSSP, P07130, 1DLC.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008979; Gal.bind_like.
Pfam, PP00555; endotoxin_l.
Pfam; PP03944; endotoxin_l.
Pfam; PP03945; endotoxin_l.
                                                                                                                                                                                                                                                                                                                     MEDLINE=94100786; PubMed=7764305;
                                                                                                                                                                                                                   CRYSCA OR CRYVIIIC(A) OR CRYIII.
                                                                                                                                                                                                                                                                                                                                                                                                           Curr. Microbiol. 28:15-19(1994).
                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       STRAIN-Buibui;
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Best Local Simi
Matches 767;
                                                                                                   BACTP
                                                                                                                                                                                                       protein)
                                                                                                               045706;
                                                                      RESULT 2
C8CA_BACTP
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InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP03944; endotoxin_1.
Pfam; PP03945; endotoxin_C; 1.
                                                                                                                                                                                                                                     number WO9315206, 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1169 AA; 133543 MW;
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                                                                                   STANDARD;
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SEQUENCE 1169 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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-!- FUNCTION: PROMOTES COLLODOSMOTIC LYSIS BY BINDING TO THE MIDGUT
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
61 ETFIS-SSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STARIN-MARK B-1986 / PSSOC; MICHAEL B-1987 F. Poncerada L., Narva K.B.; Procees for controlling scarab pests with Bacillus thuringiensis "Procees for controlling scarab pests with Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: Toxic segment of the protein is located in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pesticidial crystal protein crysBa (Insecticidal delta-endotoxin
cryVIIIB(a)) (Crystaline entomocidal protoxin) (134 kDa crystal
protein).
CRYSBA OR CRYVIIIB(A) OR 50C(B).
                                                                                                                      84;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=132267;
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                                                                                                           S--PTSDRYMRYWAGHQISYKHIGTSSTFTQMYGTNQNLQSTSN----PDFTNYDIYKTL 410
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                                                                                                                                       GLPLNNTEYLEYWVGHSIKYRNTNASSALRRNYGT----ITSNKIKYYDLANKDIFQVR 414
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ELINQKIAEYARNKALSELEGLGNNYQLYLTALEEWKENPNGSRALRDVRNRFBILDSLF 180
                             KI TQI PVVKAHTLVSGTTVI KGPGFTGGNI LKRTSSGPLAYTSVSVKSPLSQRYRARIRY
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                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal procesin cry9Ca (Insecticidal delta-endotoxin CryIXC(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
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                                                                                                                                                                                                                                           Bacillus thuringiensis (subsp. tolworthi).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Belongs to the delta endotoxin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 51.7%; Score 3123; DB 1;
Best Local Similarity 52.3%; Pred. No. 2.8e-170;
Matches 619; Conservative 195; Mismatches 327;
1157 AA
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=BTS02618A;
MEDLINE=96141404; PubMed=8572715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 237527; CAA85764.1; -. PIR; A59380; S49247. HSSP; PO130; 1DLC. InterPro; IPR001178; Endotoxin. InterPro; IPR005638; endotoxin.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the spore coat.
                                                                                                                                                                                                                 CRYSCA OR CRYIXC(A)
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C9CA BACTO
045733;
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SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGGYVTIRDGAHQBTLTFNACDYDVNGTY 1114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | IPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTBTLTFNICDDDTGVLS 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        885 FHIDTGEIDIMENTGIWVVFKIPTTNGYATLGNLELVEBGPLSGETLERAQQQEQQWQDK 944
                                                                                  240
                                                                                                                                                                                                       301 QLTREVYTDPIVFNPPANVGLCRRWGTNPYNTPSELENAFIRPPHLFDRLNSLTISSNR- 359
                                                                                                                                                                                                                                                                        360 -PPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IRST 413
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                                                                                                                                                                                                                                                                                                                                                         461
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                                                                                                                  OYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMILLVLDLVALPPNYDTRTYPIETTA 299
                                                                                                                                                                                                                                                                                                                                         OLTREVYTDPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIBFYTTRA
                                                                                                                                                                                                                                                                                                                       GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA
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                                                 VAKIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIPGAENGPTPGEISTFYDRQVTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MKQVBDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 RTYPIETTAQLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTTLQNMNYKDYLRMSBGB-----NP
                                                                                                                                                                                                                the spore coat.
MISCELLANBOUS: Toxic segment of the protein is located in the N-
                                        16-OCT-2001 (Rel. 40, Last sequence update)
6-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry98a (Insecticidal delta-endotoxin CryIXE(a)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                          EPITHELIAL CELLS OF INSECTS.
DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1150 AA; 129895 MW; 7D6AB93D6BDC97BB CRC64;
                                                                                                                             Bacillus thuringiensis (subsp. aizawai).
Bacteria, Pirmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1433;
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the delta endotoxin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 48.64; Pred. No. 2.6e-153;
Matches 574; Conservative 197; Mismatches 364;
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 1150
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INTERPOS IRROULT/8; Endotoxin.
INTERPOS IRRO05639; endotoxin.C.
INTERPOS, IRRO05639; endotoxin N.
INTERPOS, IRRO08979; Gal_bind_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB011496; BAA34908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PP03944; endotoxin_C; 1. Pfam; PP03945; endotoxin_N; 1.
                            16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP00555; endotoxin; 1.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Foxin; Sporulation.
                                                                                                              CRY9EA OR CRYIXE (A)
                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=SSK-10;
                                                                                                                                                                                                                                                                                                                                                     terminus.
C9EA BACTA
Q9ZNL9;
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-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BPITHELIAL CELLS OF INSECTS.
-i- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part the spore coat.
-i- MISCELLANBOUS: Toxic segment of the protein is located in the N-

Abano S.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

FROM N.A.

SEQUENCE

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PGMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NANSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSA 1125
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                                                                                                                                                                                                                                                                                                                                                 692
                                                                                                              PQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTID 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIDTGRIDLNENTGIWVVFKIPTTNGYATLGNLELVERGPLSGETLERAQQQEQQWQDKM 945
                                                          355 RLTISRNRYTAPTTNS-PLDYWSGHTLQSQHANNPTTYBTSYGQITSN-TRLFNTTN-GA
                                                                                                                                                                                                                                                                                           TISFVVNLFVNNSAA---GFTLPSTMAQNGSLTYESFNTLEVTHTIRFSQSDTTLRLNIF
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                                                                                                                                                                                                                           TQLPWVKASBIGGGTTVVKGPGPTGGDILRRTDGGAVGTIRANNAPLTQQYRIRLRYAS
                                                                                                                                                                                                                                                                                                                     SPASGGEVYVDKPELIPVNATPEAEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRANQI VKNVPDNLLPDVLPVNSCGGI DRCSEQQYVDANLALENNGENGNMSSDSHAFSF
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein cry9ba (Insecticidal delta-endotoxin CryIXD(a)) (Crystaline entomocidal protoxin) (132 kDa crystal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 QSLTQTYTNHCVTAYNDGLAELRGTTABSWPKYNQYRREMTLTAMDLVALFPYYNLRQYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTFIS-SSTVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLIDOKI TDSVRKTALAGLOGLGDGLDVYOKSLKNMLENRNDTRARSVVVTQYIALELDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

44.9%; Score 2715; DB 1; Length 11
Best Local Similarity 46.9%; Pred. No. 5.3e-147;
Matches 558; Conservative 204; Mismatches 383; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1169 AA; 132228 MW; 659AB257229DE5E9 CRC64;

    -!- SIMILARITY: Belongs to the delta endotoxin family.

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InterPro; IPR005638; endotoxin.C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin, 1.
Pfam; PP03944; endotoxin, C; 1.
Pfam; PP03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D85560; BAA19948.1; -. HSSP; P07130; IDLC.
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SEQUENCE 1169 AA
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protein). CRY9DA OR CRYIXD(A). Bacillus thuringiensis (subsp. japonensis). Bacteria; Firmicutes; Bacillales; Bacillus.

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"Cloning of a novel crystal protein gene crylk from Bacillus
"Cloning of a novel crystal protein gene crylk from Bacillus
"Lintingiensis subsp. morrison!";

FEMS Microbiol. Lett. 134.159-164 (1959).

-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BPITHELIAL CELLS OF INSECTS. SELECTIVELY TOXIC TO ARTOGEIA RAPAE
AND NOT ACTIVE ON PLUTELLA XYLOSTELLA.

-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part of
                                             DEEDLIHYHKVHLVKNVPDNLVSDTYSDGSCSGMNRCEBQQMVNAQLETEHHHPMDCCE
                                                                                                                                                                                                                                                                                                                                                                                                                            RNSTDBLPSLNPEGD-IIRNYSHRLSHITQYRPQATQSGSPSTVSANLPTCVWTHRDVDL
                                                                                           YRARIRYASTTNI.RI.PVTISGTRIYSINVNKTMNKGDDL.TPNTPDLATIGTAFTPSNYSD
                                                                                                                                                         SLTVGADSPASGGEVYVDKPELI PVNATPEAEEDLDVAKKAV-NGLPTSKKDALQTSVTD
                                                                                                                                                                                                                                                                                   STGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQ
                                                                                                                                                                                                                                                                                                                                                                                                             SSDSHAPSPHIDTGEIDLNENTGIWVVPKI PTTNGYATLGNLELVEEGPLSGETLERAQQ
                                TWTVYSDKITOI PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQR
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30-WAY-2000 (Rel. 39, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylKa (Insecticidal delta-endotoxin
CTYIK(a)) (Crystaline encomocidal protoxin) (137 kDa crystal protein)
CRYIKA OR CRYIK(A) OR CRYIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYDVNGTYVNDNSYITEEVVPYPETKHAMWVEVSESEGSFYIDSIRFIETQE 1169
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1441;
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SEQUENCE PROM N.A.
STRAIN=F190;
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Q45715;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LI-DQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
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                   is located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7CAP7A3311893D9B CRC64;

    -!- SIMILARITY: Belongs to the delta endotoxin family

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
44.9%; Score 2714; DB 1;
Best Local Similarity 46.3%; Pred. No. 6.4e-147;
Matches 581; Conservative 194; Mismatches 351;
                        of the protein
                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001178; Endotoxin,
InterPro; IPR005638; endotoxin_C.
InterPro; IPR0086539; endotoxin_N.
InterPro; IPR008979; Gal_bind_Tike.
Pfam; PP00555; endotoxin, 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
the spore coat.
MISCELLANEOUS: Toxic segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin; Sporulation.
SEQUENCE 1215 AA; 137378 MW;
                                                                                                                                                                                                                                                                                                                                    U28801; AAB00376.1; -. P02965; ICIY.
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                                                                                                                                                                                                                                                                                                            946 ARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEI 1005
                                                                                                                                                                                                                                                                                                                                                                        PGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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1100 TVTCNDYTTNQSAEGSTDACNSYNRGYEDGYENRYBPNPSAPVNYTPTYERGMYTDTQGY 1159
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30-MAY_2000 (Rel. 39, Last sequence update)
30-MAY_2000 (Rel. 39, Last annotation update)
30-MAY_2000 (Rel. 39, Last annotation update)
Pesticidial crystal protein crylBb (Insecticidal delta-endotoxin CrylB(b)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYIBB OR CRYIBE(B) OR CRYETS.
Bacillus thuringlensis Bacillales; Bacillaceae; Bacillus.
NCDI_TAXID=1428;
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                                                                            SDEFCLDKKRELLEEVKYAKRLSDERNILQDPTFTSISGQTDRGWIGSTGISIQGGDDIF
                                                                                                                      KENYVELPGT--VD-ECYPTYLYOKIDESQLKSYTRYQLRGYIEDSQDLEIYLIRYNAKH
                                                                                                                                                                                                    EVYVDKFELI PVNATPEAEEDLDVAKKAVNGLFTSKKD-ALOTSVTDYQVNQAANLVECL
                SDBLYPNBKRMLWDAVKBAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLF
                                                                                                                                                                                    IVKNVPDNLLP----DVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMS-SDSHAFSF
                                                                                                                                                                                                                                                                                                                                           920 EKLOLETKRVYTEAKESVDALFVDSQYDKLQANTNIGIIHGADKQVHRIREPYLSELPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                     NWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYV1 IRDGANQTETLTFN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --ICDDDTGVLSADQTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;
"Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins
toxic to lepidopteran insects".

Patent number US5322687, 21-JUN-1994.

-!- PUNCTION: PROWOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BETHTHELIAL CELLES OF MANY LEPIDOPTERAN LARVAE.

-!- DEVELOPMENTAL STRAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                                                                                                                                                                                    Indels 140;
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                                                                                                                                                                        A4C949DB675C3269 CRC64;
                                                                                                                                                                                            Query Match
42.2%; Score 2552; DB 1;
Best Local Similarity 43.2%; Pred. No. 1.1e-137;
Matches 548; Conservative 205; Mismatches 375;
                                                                            InterPro; IRR001178; Endotoxin.
InterPro; IRR005639; endotoxin.C.
InterPro; IRR005639; endotoxin.N.
InterPro; IRR008979; Gal_bind_like.
Pfam; PP00555; endotoxin.1.
Pfam; PP03944; endotoxin.C; 1.
Pfam; PP03945; endotoxin.N; 1.
                                                                                                                                                            Toxin; Sporulation.
SEQUENCE 1229 AA; 139769 MW;
                                                        EMBL; L32020; AAA22344.1;
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BENTHELLAL CELLS OF INSECTS.

DEVELOPMENTAL STARGE: The crystal protein is produced during sportlation and is accumulated both as an inclusion and as part of
                                                                                                             -ENGWICSTGIEVARGDVLPKDRSLRLTSARRIDTETYPTYLYQQIDESLLKPYTRYKLK
                        GFIGSSQDLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANLA
                                                                                                                                                                    LENNGENG-MASSDSHAPSFHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLELVBEGP
                                                                                                                                                                                           LSGETLERAQQQEQQWQDKWARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDML
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
Pesticidial crystal protein crylba (Insecticidal delta-endotoxin Crylb(a)) (Crystaline entomocidal protoxin) (140 kDa crystal protein)
CRY1BA OR CRYPIS(A) OR CRYA4.
Bacillus thuringiensis (subsp. kurstaki), and Bacillus thuringiensis (subsp. entomocidus).
Bacteria, Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=B.t.kurstaki; STRAIN=HD-2; MEDLINE=88203216; PubMed=3362680; Brizzard B.L., Mhiteley H.R.; Brizzard B.L., Whiteley H.R.; Mvcleotide sequence of an additional crystal protein gene cloned from Bacillus thuringiensis subsp. thuringiensis."; Nucleic Acids Res. 16:2723-2723(1988).
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Soetaert P.;
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It is produced through a collaboration
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42.1%; Score 2547.5; DB 1; Length 1228;
Best Local Similarity 43.8%; Pred. No. 2e-137;
Matches 558; Conservative 183; Mismatches 381; Indels 151;
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C8E3A19FB5D98575 CRC64;
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HSSP, P07130; 10DC.

HSSP, P07130; 10DC.

InterPro; IRR001178; Endotoxin.

InterPro; IRR005638; endotoxin.

InterPro; IRR008979; endotoxin.

Fram; PP00555; endotoxin.

Pfam; PP00555; endotoxin.

Pfam; PR03944; endotoxin.

Foxin; Sporulation.

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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last amonotation update)
Pesticidial crystal protein crylBc (Insecticidal delta-endotoxin CrylB(c)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYIB(C)) (CRYIB(C) OR CRYIBC.
Bacillus thuringlensis (subsp. morrisoni).
Bacteria, Firmicutes, Bacillales, Bacillus.
                                                             BCLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN-------
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"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
"Cloning of novel Bacillus thuringiensis delta-endotoxin.";
Submitted (NOV-1994) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
BENTHELLAL CELLES OF INSECTS.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during
sporulation and is accumulated both as an inclusion and as part (
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MISCELLANEOUS: Toxic segment of the protein is located in the N-
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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41.2%; Score 2491; DB 1;
Best Local Similarity 42.1%; Pred. No. 3.4e-134;
Matches 536; Conservative 208; Mismatches 384;
                                                                                       InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR0086539; endotoxin_N.
InterPro; IPR008979; endotoxin_N.
Pfam; PP00555; endotoxin_1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_N; 1.
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                                                                                                                                                                                                                                              NATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGA 1105
                                                                                                                                                                                                                                                                                                                                                -----LSADQTSYITKTVEFTPSTEQV#IDMSETEGVF 1155
                                                            SEQUENCE FROM N.A.
STRAIN=NRRL B-18872 / PS158C2;
STRAIN=NRRL B-18872 D.A., Cannon R.J.C., Narva K.E., Stelman S.;
Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;
"Bacillus thuringiensis genes encoding lepidopteran-active toxins.";
Patent number US5723759, 03-MAR-1998.
-! FUNCTION: PROMOTES COLLOIDOSMOTIC INSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF MANY LEPIDOPTERAN LARVAR.
-! DRVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                            - ENGWTGSTGI BVAEGDVLFKDRSLRLTSARBI DTBTYPTYLYQQI DESLLKPYTRYKLK
              GPIGSSODLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQ----YVDANLA
                                                                                                                                              LSGETLERACCOGECCWODKWARKRGASEKAYYAAKQAIDRLFADYQDCKLNSGVEMSDML
                                                                                                LENNGENG-NMSSDSHAFSFH1DTGE1DLNENTGIWVVFK1PTTNGYATLGNLELVEEGP
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 Crystal protein crylBe (Insecticidal delta-endotoxin
CrylB(e)) (Crystaline encomocidal protoxin) (139 kDa crystal protein)
CRYlBE OR CRYIB(B) OR 158C2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the spore coat.
MISCELLANEOUS: Toxic segment of the protein is located in the N-
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1222 IVDSVBLLLMBE 1233
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                                                                                                                                                                                                                                           Indels 134;
                                                                                                                                                                                                      Length 1227;
                                                                                                                                                                        CBA847BEA0B34CD3 CRC64;
                                                                                                                                                                                                      Query Match
40.7%; Score 2462; DB 1;
Best Local Similarity 42.9%; Pred. No. 1.5e-132;
Matches 542; Conservative 196; Mismatches 392;
                            InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR0085639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP003555; endotoxin; 1.
Pfam; PP03944; endotoxin_C; 1.
Pfam; PP03945; endotoxin_C; 1.
Toxin; Sporulation; Plasmid.
                                                                                                                                                                      139084 MW;
AAC32850.1;
                                                                                                                                                                        1227 AA;
AF077326; AA
P07130; 1DLC
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                                                                              923
                                                                                                         930 TLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQN 989
                                                                                                                      MEDLINE=92384571; PubMed=1514800;
MEDLINE=92384571; PubMed=1514800;
Lambert B., Hofte H., Annys K., Jansens S., Soetaert P., Peferoen M.;
Lambert Bacillus thuringiensis insecticidal crystal protein with a
silent activity against coleopteran larvae.";
Appl. Environ. Microbiol. 58:2536-2542(1992).
-!- FUNCTION; PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
EPITHELIAL CELLS OF COLEOPTERA. THIS PROTEIN IS NOT TOXIC IN ITS
NATURAL PORM. IT IS HIGHLY TOXIC TO COLORADO POTATO BEETLE LARVAE
AFTER AN IN VITRO SOLUBILIZATION AND TRYPSIN ACTIVATION STEP.
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                                                                  CRDGERCAHISHHESLDIDVGCIDLHENLGVWVVFKIKTQBGHARLGNLBFIEEKPLLGB
                                                                                                                                                                             SSODLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSBQQYVDANLALENN
                DSQDLRIYLIRYMAKHETLDVPGTESVWPLSVESPIGRCGEPNRCA--PHFEWNPDLDCS
                                                      GENG-NMSSDSHAPSPHIDTGEIDLNENTGIWVVPKIPTTNGYATLGNLRLVEEGPLSGE
                                                                                                                                                                                                                                                                                               1104 BLKFKNCEBEEVYPTDTGTCNDYTAHQGTAACNSRNAGYEDAYEVDTTASVNYKPTYEEB
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30-MAY-2000 (Rel. 39, Last amoutation update)
Pesticidial crystal protein cry7Aa (Insecticidal delta-endotoxin CryVIIA(a)) (Crystaline entomocidal protoxin) (129 kDa crystal
                                                                                                                                                                                                                                                                    1110 TLIPNICDD-----PRGVLS------ADQTS---
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
NCBI_TaxID=1428;
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                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                     Match 40.7%; Score 2458.5; DB 1; Local Similarity 43.5%; Pred. No. 2.2e-132; es 514; Conservative 208; Mismatches 400;
                                                                        InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PR00555; endotoxin; 1.
Pfam; PR03944; endotoxin_C; 1.
                                                                                                                                                                               Pfam; PF03945; endotoxin_N; 1.
Toxin; Sporulation.
SEQUENCE 1138 AA; 129391 MM
M64478; AAA22351.1;
A07236; CAA00646.1;
                                    PIR; A48944; A48944.
HSSP; P07130; 1DLC.
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Toxin; Sporulation. SEQUENCE 1138 AA;
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                                                                                                                                                                                                                                                                                             1066
                                                                                                                                                                                                                                                                                                                     947 RKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIP 1006
                                                                                                                                                                                                                                                                                                                                                                                    WNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSAD 1126
                                                                                                                                                                                                                                                                                                                                                                                                            DAKHRILDVSDNILPDILPENTCGEPNRCAAQQYLDENPSPECSSMQDGILSDSHSPSIN 856
                                                                                                                                      Payme J.M., Fu J.M.;
Payme J.M.;
Payme J.M.;
"Coleopteran-active Bacillus thuringiensis isolates and genes encoding coleopteran-active toxins.";
Patent number USS28646, 15-FEB-1994.
-!- PUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT EPITHELIAL CELLS OF COLEOPTERA.
-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                     RANQIVKNVPDNILLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNASSDSHAPSFH
                                                                                                                                                                                                                             GMNYTSFTELTNRLQQAWNLYDLRNA! PNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPN
                                                                                                              I DTGE I DLNENTG I WVVFKI PTTNGYATLGNLELVEBGPLSGETLERAQQQBQQWQDKMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: Toxic segment of the protein is located in the N-
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16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis (subsp. dakota).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=132268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1096 ISGYITXELEFFPDTEKVHIBIGETEGIFLVESIELFLARE 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1127 QTSYITKTVEFTPSTEQVWIDMSBTEGVPNIBSVELVLEBE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the delta endotoxin family.
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InterPro; IPR005639; endotoxin_N.
InterPro; IPR008979; Gal_bind_like.
Pfam, PF00555; endotoxin_1.
Pfam; PF03944; endotoxin_C; 1.
Pfam; PF03945; endotoxin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001178; Endotoxin.
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CRY7AB OR CRYVIIA(B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 YKAFSHBIQPDLFYWCVHKVSFKKSBQSNLYTTGIYGKTSGYISSGAYSFRGNDIYRTLA 398
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                                                                              Gaps
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01DF7072C074CB88
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                                   tch 40.7%; Score 2458.5; DB 1; al Similarity 43.1%; Pred. No. 2.2e-132; 512; Conservative 218; Mismatches 384;
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1033 NGDFNNGLSCWNVKGHVDVQQSHHRSDLVIPEWRABVSQAVRVCFGRGYILRVTAYKBGY 1092
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         241 YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLYLDLVALFPNYDTRTYPIBTTAQ 300
227 YSNHCVQWYNTGLNNLRGTNABSWLRYNQFRRDLTLGVLDLVALFPSYDTRTYPINTSAQ 286
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                                                                                      LIDOKI TDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYI ALBLDFV
                                                                                                                                181 AKIPSPAISGOEVPLLSVYAQAANLHLLLRDASIPGAEWGFTPGEISTPYDRQVTRTAQ
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                             1029 NNVLVLANNDAQVLRAVKLYQDRGYVLRVTARKIGIGEGYITITDERGHTDQLRFTAC-B 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
TKWRNKLACMTTETQAIYTRAKQALDNLFANAQDSHLKIDVTFABIAAARKIVQSIREVY 968
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                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Pesticidial crystal protein crylBd (Insecticidal delta-endotoxin
CrylB(d)) (Crystaline entomocidal protoxin) (140 kDa crystal protein).
CRYIBD OR CRYIB(D) OR CRYLAI OR CRYEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             part of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=HD-525;
MEDLINE=20153386; PubMed=10688690;
Kuo W.-S., Lin J.-H., Tzeng C.-C., Kao S.-S., Chak K.-F.;
"Cloning of two new cry genes from Bacillus thuringiensis subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as I
                                                                                                                                                                     DTGVLSADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEBE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Microbiol. 40:227-232(2000).
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE N
EPITHELIAL CELLS OF LEPIDOPTERAN LARVAE. TOXIC TO PLUTELLA
XYLOSTELLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 205; Mismatches 377; Indels 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1231 AA; 139654 MW; 129A0371CDDBEE52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Bacillus thuringiensis (subsp. wuhanensis).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=52024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminus. Selongs to the delta endotoxin family.
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                                                                                                                                                                                                                                                                 1231 AA
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InterPro; IPR005638; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal bind like.
Pfam; PP00555; endotoxin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03944; endotoxin_C; 1. Pfam; PF03945; endotoxin_N; 1. Toxin; Sporulation.
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                                                                                                                                                                                                                                                                 STANDARD;
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Matches 537
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GASEKAYYAAKQAIDRLPADYQDQXINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMN 1009
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                                                               PLSRGYSHRLSHITSYSPSKNASSPARYGN--LPVPAWTHRSADVTNTVYSDKITQIPVV
                                        LIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDFV
                                                                                                                  341 APSHBIQPDLFYWSAHKVSFKQSBQSNLYTTGIYGKTSGYISGAYSFRGNDIYRTLAAP
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NT----AINTVVSVTGATLSALGVPGASPITNFYLKITGLLWPHDK-NIWDBFMTBVBT
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| TASVNYKPTYBBETYTDVRRDNHCGYDRGYVNYPPVPAGYVTKBLBYFPBTDTVWIBI 1212
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                             -----YITKTVEFTPSTEQVWIDM
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"Coleopteran-active Bacillus thuringiensis isolates and genes encodir "Coleopteran-active toxins.";
Patent number US5286486, IS-FEB-1994.
-!- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT BETHERIZAL CELLS. OP COLEOPTERA.
-!- DEVELOPMENTAL STACE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MISCELLANEOUS: Toxic segment of the protein is located in the N-
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                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CryVIIA(b)) (Crystaline entomocidal protoxin) (130 kDa crystal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.4%; Score 2439.5; DB 1; Length 1138;
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nes 510; Conservative 210; Mismatches 402; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1138 AA; 129658 MW; B12DC80C0A56D1DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis (subsp. kumamotoensis).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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Interpro; IPR005638; endotoxin_C.
Interpro; IPR005639; endotoxin_N.
Interpro; IPR008979; Gal_bind_like.
Pfam; PF00555; endotoxin; 1.
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1213 GETEGKFIVDSVELLIMEE 1231
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                                                                                                                                                                  SETECVFNIESVELVLEER
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                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                    DOTS
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SEQUENCE 1138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=132267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Search completed: June 21, 2004, 13:37:53 Job time : 23 secs

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STRAIN-SDS-502;
A RAINO S., Yanamoto T.;
Anamoto T.;
Anamoto T.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB089299; BAC07226.1; -.
GO; GO:0010592; P:defense response; IRA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin.
InterPro; IPR006539; endotoxin.
InterPro; IPR008979; Gal bind_like.
Fram; PF00555; endotoxin.
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Fram; PF00555; endotoxin.
Fram; PF00944; endotoxin.
Fram; PF00944; endotoxin.
Fram; PF00944; endotoxin. N.;
Fram; PF00945; endotoxin. N.;
Fram; PF00945; endotoxin. N.;
SEQUENCE 1144 AA; 128060 MW; 98F93070C4901AAB CRC64;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29338;
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Copyright (c) 1993 - 2004 Compugen Ltd.
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77 PLWPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQNYYNQYLIALKEWEBRPN 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE-94085596; PubMed-826221;
WEDLINE-94085596; PubMed-8262221;
WEDLINE-94085596; PubMed-8262221;
WEDLINE-94085596; PubMed-8262221;
WEDLINE-94085596; PubMed-8262221;
Chestukhina G.G., Stepanov V.M.;
Chestukhina G.G., Stepanov V.M.;
The state of the cryX**-the novel Delta-endotoxin-related of the cryX*-the novel Delta-endotoxin-related of t
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45.5%; Score 2750.5; DB 2; Length
Best Local Similarity 48.7%; Pred. No. 2.8e-148;
Matches 562; Conservative 197; Mismatches 341; Indels
                                                                                                                                                                                                                                                                                                                                                  Bacillus thuringiensis.
Bacceria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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      1118 TEQVWIDMSETEGVFNIESVELVLEEE 1144
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O45745

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DT 01-NOV-1996 (TERMELTEL) 01, CX

O1-OCT-2003 (TERMELTEL) 01, LB

D1 01-OCT-2003 (TERMELTEL) 01, LB

D1 01-OCT-2003 (TERMELTEL) 01, LB

D2 01-OCT-2003 (TERMELTEL) 01, LB

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                                                                                           LIDOKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
                                                                                                                              LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV
                                                                                                                                                                                                                                                                                                                                        YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIBTTAQ
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KGFIGSSQDLBIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRCSEQQYVDANL 865
                                                                                                                                                                                                                                                                                                                         61 BTFISSSTVQTGIGIVGQVLGALGVPPAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVBD 120
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                                                                                                                                                                                                                                                                                                                                                282 LTREVYTDAIGATGVNWASM--NWYNNNAPSPSAIBAAAIRSPHLLDFLEQLTIPS--AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 SRWSNTRIMITWRGHTIQSRPIGGGLNTSTHGATNTSINPVTLR-----PASRDVYRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               415 SLGADL---ANYYAQVYGVPYASFILLDKOVIGSGSVGGFTYSKPHTTMQVCTQNYNTIDBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 TNERLFVTISGTRIYSINVNKTWNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   681 ACLSDEPCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHE
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                                                                                                                                                                                                                                      MSPNNQNEYRILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPBLFGNP
                                                                                                                                                                                                                                                                 ch 42.1%; Score 2545.5; DB 2; Length 1228; ll Similarity 43.8%; Pred. No. 1.6e-136; S58; Conservative 183; Mismatches 381; Indels 151;
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1228 AA; 139621 MW; 3DA2A4DBF59C95C3 CRC64;
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                        LKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLPVTISGTRIYSINVNKTMNKGD
        NASSPARYGNLPVPAMTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKGPGPTGGNI
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"Characterization of crylB gene and its flanking regions cloned from
"Characterization of crylB gene and its flanking regions cloned from
Bacillus thuringiensis subsp. entomocidus HD-9.";

Bubmitted (MAR.2001) to the BMBL/GenBank/DDBJ databases.

EMBL, AF363025, AAK51084.1;

GO; GO:0015070; P:toxin activity; IRA.

GO; GO:0015070; P:toxin activity. IRA.

InterPro; IPR001179; Endotoxin.

InterPro; IPR005638; endotoxin._C.
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Bacillus thuringiensis (subsp. entomocidus).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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01-OCT-2003 (TrEMBLrel. 25,
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                                LTREVYTDPIVPNRETSGGFCRRWSLNSDISPSEVESAVIRSPHLPDILSEIBFYTTRAG
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                                     PLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLMSGVEMSDM 984
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42.0%; Score 2539.5; DB 2; Length 1228;
Best Local Similarity 43.8%; Pred. No. 3.5e-136;
Matches 557; Conservative 183; Mismatches 382; Indels 151;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

RMBL, AP768257; AAK53251.1;

GO; GO:0006952; Pidefense response; IEA.

InterPro; IPR001178; Endotoxin.C.

InterPro; IPR005639; endotoxin.N.

InterPro; IPR005639; endotoxin.N.

InterPro; IPR008979; Gal_bind_like.

Pfam; PP00355; endotoxin I.

R Pfam; PP003944; endotoxin N; 1.

R Pfam; PP003945; endotoxin N; 1.

R Pfam; PP003945; endotoxin N; 1.
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CRY1BA.
Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1428;
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Q93NM5;
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01-DEC-2001 (TEMBLE1.19,
01-OCT-2003 (TEMBLE1.25,
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975 INSGVEMSDMIAAQNIVQSIPYVYNDALPRIPGMNYTSPTELTNRLQOAWNLYDLRNAIP 1034
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                                                                                                                                                                           800 LLKPYTRYKLKGFIGSSODLEIKLIRHRANQIVKNVP--DNLLPDVL--PVNSCGGIDRC
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                       YRARIRYASTTNI.RLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSD
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SEQUENCE FROM N.A.
Meza-Basso L.A., Theoduloz C.;
Meza-Basso L.A., Theoduloz C.;
"Cloning and expression of a delta endotoxin gene from a Chilean
native Bacillus thuringiensis strain.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94191; AAG16877.1; -.
PIR; A29125; A29125.
HSSP; P02965; LCIY.
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
MCBI_TaxID=1428;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
532 IPVVKAHTLVSGTTVIKGPGFTGGNILKRTSSG-
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1213 GETEGKFIVDSVELLLMBE 1231
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"Cloning of a novel Bacillus thuringiensis cryIBII gene for insecticidal crystal protein.";

"Insecticidal crystal protein.";

Insecticidal crystal protein.";

EMBL; AX138457; AAM93496.1; --:

R GO; GO:0010590; Ptoxin activity; IEA.

R GO; GO:00106952; Predense response; IEA.

InterPro; IPR005639; endotoxin. C.

R InterPro; IPR008639; endotoxin. N.

InterPro; IPR008939; endotoxin. N.

R Pfam; PF003946; endotoxin. 1.

Pfam; PF03945; endotoxin. N; 1.

Pfam; PF03945; endotoxin. N; 1.

R Pfam; PF03945; endotoxin. N; 1.

SEQUENCE 1231 AA; 139765 WW; C9P2848A9297EA00 CRC64;
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                                                                                                                                                                                                                        CRÝIBII.
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428;
                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                  Created)
                                                                                                        QBKNY2;
01-OCT-2002 (TIEMBLEEL 22,
01-OCT-2002 (TIEMBLEEL 22,
01-OCT-2003 (TIEMBLEEL 25,
                                                                                     PRELIMINARY;
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AC QBRNY
DD 01-0
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DR CCYJI
GS BACH
OC NCBI
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EMSDMLAAQNIVQSI PYVYNDALPBI PCANYTSFTBL TNRLQQAWNLYDLRNAI PNGDPR
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                                                                                    LVEEGPLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGV
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Nagamateu Y., Itai Y., Hatanaka C., Punatsu G., Hayashi K.;
*A Toxic Pragment from the Entomocidal Crystal Protein of Bacillus
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Nucleotide Sequence of the Lepidoptera-toxic Protein Gene
thuringiensis subsp. dendroliwus T94Al.";
J. Pac. Appl. Biol. Sci. Hiroshima Univ. 29:95-107(1990).
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SPECIES=B.thuringiensis (subsp. sotto);
Zhong S.K., Xiang Y.W.;
Zhong W.F., Cai P.Z., Yan W.Z., Zhang Z.X., Xiang Y.W.;
*A crylA gene cloned from Bacillus thuringiensis serovar is
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB026261; BAA77213.1;
EMBL; APS10713; AAM44305.1;
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Bacillus thuringiensis, and
Bacillus thuringiensis (subsp. sotto).
Bacteria; Pirmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1428, 29340;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
BtT84Al crystal protein (Crystal protein CrylA).
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GO, GO:0006952; P:defense response; IBA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005638; endotoxin_C.
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SPECIES=B.thuringiensis; STRAIN=T84A1;
Nagamatsu Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
SPECIES=B.thuringiensis; STRAIN=T84A1;
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HSSP; P02965; 1CIY.
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GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0006952; Pidfeinea response; IEA.
InterPro; IPR00178; Endotoxin.
InterPro; IPR00539; endotoxin.C.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR008679; Gal.bind_like.
Pfam; PF00955; endotoxin,1.
Pfam; PF003944; endotoxin,2.
Pfam; PF03944; endotoxin,N; 1.
SEQUENCE 1155 AA; 130557 MW; 5D69E3E2P527749D CRC64,
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                                 QKLNSGVEMSDMLAAQNIVQSIPYVYNDALPBIPGMYYTSFTELTNRLQQAWNLYDLRNA
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=1y30;
Yao J., Zhang J., Song F., Chen Z., Li C., Huang D.;
Yao J., Zhang J., Song F., Chen Etrain 1y30.";
"A novel crylda gene from Bt strain 1y30.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF384211; AAP80146.1;
SEQUENCE 1176 AA; 133169 WW; 725C14EA940B869B CRC64;
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Last annotation update)
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Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1428;
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                                                                                                               33.9%; Score 2050; DB 2; Length 1180; 39.3%; Pred. No. 3e-108;
                                                                                                                                Best Local Similarity 39.3%; Pred. No. 3e-108;
Matches 481; Conservative 173; Mismatches 414; Indels
   InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00555; endotoxin; 1.
Pfam; PP03944; endotoxin C; 1.
Pfam; PP03945; endotoxin N; 1.
SEQUENCE 1180 AA; 133489 MW; 1199E4A6D1DCE62D CRC64;
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                                                                 PS-----TIYRQRGTV------DSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAV
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(TrEMBLrel. 25, Last annotation update)
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus. NCBI_TaxID=1428; [1]

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STRAIN=FU-2-7;
Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
"Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from Bacillus thuringiensis var. kurstaki HD-1 DNA.";
Agric. Biol. Chem. 51:455-463(1987).
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965 965 S -> P (IN REP. 1).
1976 AA; 133075 WW, AA4135849A289PBS CRC64;
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MEDLINE=94289859; PubMed=7764972;
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Hou B.K., Chen Z.H.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFI194676; AAD55382.1; -.
HSSP; P02965; ICIY.
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Bacillus thuringiensis (subsp. kurstaki).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=29339;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GO; GO:0006952; P:defense response; IEA.
InterPro; IPR001179; Endotoxin.C.
InterPro; IPR005639; endotoxin.C.
InterPro; IPR008639; endotoxin.N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PF00555; endotoxin.1.
Pfam; PF00344; endotoxin.C; I.
Pfam; PF03445; endotoxin.N; I.
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                             Ouery Match 33.7%; Score 2034; DB 2; Length 1176; Best Local Similarity 39.2%; Pred. No. 2.4e-107; Matches 478; Conservative 173; Mismatches 417; Indels 152;
1176 AA; 133010 MW; PCBE069D0B81D8C4 CRC64;
 SEQUENCE
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980 EMSDMLAAQNIVQSIPYVYNDALPRIPGMNYTSPTELTNRLQQAWNLYDLRNAIPNGDFR 1039
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                                                                                                                                                                                                                                                                                                  504
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                                                                                                                                                                                             LPSAVYRKSGTV-----DSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSI
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AVIRSPHIPDILSBIBPYTTRAGLPLANTEYLBYWYGHSIK----YKNTNASSALERNY
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01-JUL-1997
01-OCT-2003
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DTGVLSADQTS-----YITKTVEFTPSTEQVWID 1147
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Yu J., Tan L., Wu D., Pang Y.;
"Molecular characterization of a silent gene encoding a 130-kilodalton crystal protein from Bacillus thuringiensis subsp. israelensis.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR375608; AAK55546.1; -.
                                                                                                             4 NPNINECI PYNCLSNPEVBYLGGERIETGYTPIDISLSLYQFLLSEFVPGAGFVLGLVDI
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                                                                                    EGVGDGYVIIRDGANQTETLTFN------ICDD------
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GO; GO:0006952; P:defense response; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR005639; endotoxin C.
InterPro; IPR005639; endotoxin N.
InterPro; IPR008979; Gal_bind_like.
Pfam; PP00355; endotoxin; 1.
Pfam; PP03944; endotoxin; 1.
Pfam; PP03944; endotoxin; 1.
Pfam; PP03945; endotoxin; N; 1.
SEQUENCE 1155 AA; 130747 MW; 7F0C98E0100C7698 CRC64;
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01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-DCT-2003 (TEMBLrel. 25, Last annotation update)
Crystal protein CrylAbl6.
CRYIAB16.
Bacillus thuringiensis (subsp. israelensis).
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508 INSPITQRYRLRFRYASSRDARITVAIGGQIRVDWTLEKTMEIGESLTSRTFSYTNFSNP
                                                                                  692 ALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRIN-
                                                                                                                                                                                                                                                                         -GENGWICSTGIEVARGDVLFKDRSLRLISAREIDTETYPTYLYQQIDESLLKPYTRYKL
                                                                                                                                                                                                                                                                                                                                                                                      810 KGPIGSSODLEIKLIRHRANQIVKNVPDN----LLPDVLPVNSCGGIDRCSEQQYVDANL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  866 ALE-INGENGINSSDSHAFSFHIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVEEG
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                                                         PTFSNYSDSLTVGADSPASGGEVYVDKFBLIPVNATFRAEBDLDVAKKAVNGLFTSKKO-
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-B-Pr-88;

L. C., Zhang J., Li G., Huang D.;

"A crystal endotoxin from Bt strain.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF288683; AAO13756.1;

EMBL; AF288683; AAO13756.1;

ROG; GO:0006952; P:defense response; IEA.

R GO; GO:0006952; P:defense response; IEA.

R InterPro; IPR0051178; Endotoxin. C.

R InterPro; IPR005639; endotoxin. C.

R InterPro; IPR005639; endotoxin. N.

R InterPro; IPR00555; endotoxin. I.

R Pfam; PF00555; endotoxin. 1.
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Bacillus thuringiensis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
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Barboza-Corona J.B., Lopez-Meza J.B., Ibarra J.E.;

"Cloning and expression of the crylEad gene of Bacillus thuringiensis and the comparative toxicity of its gene product.";

World J. Microbiol. Biotechnol. 14:437-441(1998).
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HSSP; P02965; 1CIX.
G0; G0:00105010; P:tefense response; IEA.
G0; G0:0006952; P:defense response; IEA.
InterPro; IPR001178; Endotoxin.
InterPro; IPR006539; endotoxin.C.
InterPro; IPR006539; endotoxin.N.
InterPro; IPR008979; Gal bind like.
Ffam; PF00555; endotoxin.1.
Ffam; PF03944; endotoxin.N.
Ffam; PF03945; endotoxin.N.
SEQUENCE 1171 AA; 133310 MW; 333603A1A782523A CRC64;
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Bacillus thuringiensis.
Bacillais Pirmicutes; Bacillales; Bacillaceae; Bacillus.
VCBI_TaxID=1428;
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Ibara J.E., Barboza-Corona J.E.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U94323; AAD04732.1;
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960 YDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVPEWEAEVSQEVRVCPGRGYIL 1019
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                                                                                                                                 Gaps
                                                                                                                                 148;
                                                                               Length 1169;
                                                                                                                              Indels
Pfam; PF01945; endotoxin_N; 1.
SEQUENCE 1169 AA; 132990 MW; 07C9D6D180F3DB6D CRC64;
                                                                       Query Match 33.1%; Score 2003; DB 2; Best Local Similarity 39.3%; Pred. No. 1.4e-105; Matches 460; Conservative 173; Mismatches 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333
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59 NPRIPISSSTVQIG-----IGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVW 111
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
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                                                                                     IPQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTI 469
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Bacillus thuringiensis.
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                                                                              STGIEVAEGDVLFKORSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPIGSSQ 817
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Search completed: June 21, 2004, 13:39:04 Job time : 63 secs

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GenCore version 5.1.6
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June 21, 2004, 13:30:40; Search time 65 Seconds (without alignments) 5072.814 Million cell updates/sec Run on:

US-10-089-678-1 Title: Perfect :

1 MSPNNQNEYBILDASSSTSV......MSBTEGVPNIESVBLVLEEB 1167 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp20028:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* A_Geneseq_29Jan04:* 1: geneserm1000. geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STEMMARTES

	Description	Aau80281 Bacillus	Aar28900 Toxin 50C	Aar25997 Delta-end	Aar33768 Bt isolat	Aaw06418 Antiscara			Aar32354 Coleopter		Aau99256 Bacillus		Aaw06417 Antiscara	Aaw84581 Amino aci	Amino	Amino	Amino	Amino	Amino	Aaw84582 Amino act	Aaw84593 Amino aci	Amino	Aaw84578 Amino aci	Aaw84576 Amino aci	Aar48678 Insectici	Aaw84570 Amino aci
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AL I GNMENTS

Bacillus thuringiensis insecticidal protein. Insecticide; transgenic; Coleoptera larvae. AAU80281 standard; protein; 1167 AA. 03-AUG-2000; 2000JP-00236140. 30-JUL-2002 (first entry) Bacillus thuringiensis. JP2002045186-A. 12-PEB-2002.

03-AUG-2000; 2000JP-00236140.

(SDSB-) SDS BIOTECH CORP.

WPI; 2002-356468/39.

A protein having insecticidal activity, a DNA encoding said protein, and an agent and a method for preventing harmful organisms.

Claim 1; Page 9-12; 19pp; Japanese.

This invention relates to a crystalline protein comprising a fully defined sequence and the mucleotide sequence encoding this protein. The protein of the invention is an agent for preventing barmful organisms comprising Bacillus thuringlensis servova galleriae SDS502, its mutant or a microbe transformed by a DNA encoding the protein. This microbe can be used to produce a protein containing the protein, or containing a protein having insecticidal activity produced by the SDS502, its mutant or a transformed microbe, a microbe which is transformed by using the above or a seed transformed by using the above DNA, and pacific or a seed transformed by using the above DNA, and Bacillus thuringiensis servorar galleriae SDS502 producing a protein comprising and producing a protein showing insecticidal activity. The protein of the invention may have insecticidal activity. The agent is used for preventing Coleoptera larvee. This sequence represents the Bacillus thuringiensis insecticide protein of the invention

Sequence 1167 AA;

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61 BTPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSFIVGQLMPSSTVSVWEMIMKQVED 120
QQAWNI YDLRNA I PNGDFRNGLSDWNA TSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPN
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91US-00759248.
91US-00768141.
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(first entry)
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                                                                                                                                         standard;
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13-SEP-1991;
30-SEP-1991;
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25-MAR-2003
01-APR-1993
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241 YSDYCVKWYNTGLDKLKGTNAASWLKYHQFRREWILLVLDLVALPPNYDTRTYPIETTAQ 300
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                                                        MSPANQNEYETLDASSSTSVSDNSVRYPLANDQTTTLQNANYYOYLRMSEGENPELFGNP
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                                             MSPNNQNBYE1LDASSSTSVSDNSVRYPLANDOTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVED
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                                                                                             1021 QQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIPNWNSQVSQQFTVQPN
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1129 PYTDQMWIRISRTEGTFYIRSVELIVDVE 1157
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27-JAN-1993
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181 AKIPSFAISGOEVPLILSVYAQAANIHILLILRDASIFGAEWGFTPGEISTFYDRQVTRTAQ 240
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The sequence given is an approx. 130 kD protien known as Bacillus thuringiensis PS50C (B.t.PS50C). This novel delta-endotoxin has been shown to be active against the Colorado potato beetle (Leptinotarsa decemlineata). The gene encoding this toxin can be transformed into suitable hosts such as Pseudomonas, which can then be applied to the environment of coloropteran insects where they will proliferate and be ingested by the insects. This DNA sequence can be inserted into an expression vector which contains a promoter/operator region, a ribosome binding site, polyadenylation signals, etc. This will allow transcription and translation of the cells in the appropriate host. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RTF1SSST1QTGIVGR1LGALGVPFASQ1ASFYSFYVGQL#PSKSVD1WGB1MGRVBB 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                             B.t.PS50C; colorado potato beetle; Leptinotarsa decemlineata;
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                                                                                                                                                                                                                                                                                                                                                 Pseudomonas; expression vector
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AAR25997 standard; protein;
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91US-00758020 92US-00941650 92WO-US007697

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Controlling lepidopteran pests - using compsn. of Bacillus thuringiensis strains or plants or microorganisms transformed with their toxin genes.
                                                                                                                                                                                                          Claim 12; Page 22-25; 38pp; English
                                                                                                                                              KA, Bradfish GA
                                             Bacillus thuringiensis
                             Lepidopteran-active;
                                                                                                                               (MYCO ) MYCOGEN CORP.
                                                                                                                                                           WPI; 1993-100566/12.
N-PSDB; AAQ38653.
15-JUL-1993 (first
                Bt isolate Ps50C
                                                                                                         12-SEP-1991;
                                                                                          11-SEP-1992;
                                                                                                                08-SEP-1992;
                                                            W09304587-A1
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                                               YLGDTIEKNRFNKTMDNGASLTYEFFKFASFITDFOFRETODKILLSMGDFSSGGEVYID
                                                                                                                                                                                                                                                                                                                           YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYP1ETTAQ
                                      LTREVYTOPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRAG
                                                                   LPLNNTEYLEYWYGHSI KYRNT-NASSALERNYGTI TSNKI KYYDLANKDI FQVRSI CAD
                                                                            LANYYAQVYGVPYASFTLLDKYTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPPENE-P
                                                                                                                                LSRGYSHRLSHITSYSPSKNASSPARYGNLPVPANTHRSADVTNTVYSDKITQIPVVKAH
                                                                                                                                                             TLVSGTTVIKGPGPTGGNILKRISSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLPVT
                                                                                                                                                                                           599 ISGTRIYSINVNKTMNKGDDLTPNTFDLATIGTAPTFSNYSDSLTVGADSFASGGEVTVD
                                                                                                                                                                                                                                                        NEKRMI. MDAVKBAKRLVQARNI. LQDTGPNR I NGENGWTGSTGI BVAEGDVI. PKDRSLRLT
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The sequences given in AAR33768-70 represent lepidopteran-active toxins. The DNA encoding these sequences were used within a Ti or Ri plasmid, to transform plant cells. Whole plants can then be regenerated from the transformed cells. The toxin may also be produced by cloning Bacillus thuringiensis (Bt) . It may then be applied directly to the plant locus. (Updated on 25-MNA-2003 to correct PN field.) (Updated on 25-MNA-2003 to correct PN field.)
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                                                                                                                                                                                                                   Gape
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                                                                                                                                                                               Length 1157;
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                                                                                                                                                                               Match 66.3%; Score 4007; DB 2; Iocal Similarity 66.1%; Pred. No. 1.9e-255; Nes 773; Conservative 144; Mismatches 238;
                                                                                                                                                 Sequence 1157 AA;
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AAR33768

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(revised)

25-MAR-2003

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AKQAIDRLFADYQDQKINSGVEMSDMLAAQNLVQSIPYVYNDALPEIPCMNYTSFTELTN 1018
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LANYYOKAYGVPGSWFHMVKR--GTSSTTAYLYSKTHTALOGCTQVYBSSDBIPLDRTVP 477
                                                                                                                                              YLGDTIEKNRFNKTMDNGASLITYETFKRASFIIDFQFRETQDKILLSMGDFSSQGEVYID
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                                    SESTABLISHITSHSFSKNGS--AYYGSPPVFVWTHTSADLANTIYSDKITQIPAVKGD
                                                                                                                                                                                   KPELI PVNATPEAERDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAANLVECLSDELYP
                                                                                                                                                                                                 TLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                                                                                                                               ISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAPTFSNYSDSLTVGADSPASGGEVYVD
                          LSRGYSHRLSHITSYSFSKNASSPARYGNLPVFAWTHRSADVTNTVYSDKITQIPVVKAH
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Toxin 50C(a); scarab pest; toxin; insect; scarabaeidae; pest control; larval stage insect; grain; tuberous crop; white grub; chafer grub; cyclocephala; popillia.
                                                                                                                                                                         Bacillus thuringiensis; strain kumamotoensis
                                                 Ź
                                                AAW06418 standard; protein; 1157
                                                                                                                 Antiscarab pest toxin 50C(a)
                                                                                     (revised)
(first entry)
                                                                                     16-OCT-2003
28-JAN-1997
                                                                   AAW06418;
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The DNA encoding this sequence was isolated from the Bacillus
The DNA encoding this sequence was isolated from the Bacillus
The DNA encoding this sequence was isolated from the Bacillus
Thuringiensis strain knumanotensis. Insects in the family Scarabacidae
constitute a serious pest control problem, especially when destructive
larval stage insects infest high value turf found in golf courses,
playing fields and lawns. The larvae of many species also attack grains,
tuberous crops, and ornamentals. The larvae are known as white grubs, or
chafer grubs, and can be found in Geraying organic matter, or in the soil
where they consume plant roots. In Burope and the U.S. populations of
these larvae and adults have developed resistance to chemical
insecticides such as the organochlorines and DDT. These toxin sequences,
and intext cells that are capable of expressing these proteins, can be
used to control many pests of the family scarabacides, such as species of
cyclocophala, and Popillia. The toxins are active against larvae (present
in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS
field)
                                                                                                                                                                                                                                                New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae.
                                                                                                                                                Michaels TE
                                                                                                                                                                                                                                                                                                                                                  Example 2; Col 21-26; 24pp; English.
                  91US-00808316.
92US-00828430.
93US-00014941.
                                                                                                                                                Narva KB,
                                                                                                       (MYCO ) MYCOGEN CORP
                                                                                                                                                                                           WPI; 1996-424659/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1157 AA;
                                                                                                                                                                                                                  N-P6DB; AAT43222
                                                                                                                                                  Foncerrada L,
                  16-DEC-1991;
30-JAN-1992;
01-PEB-1993;
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Query Match 66.3%; Score 4007; DB 2; Length 1157; Best Local Similarity 66.1%; Pred. No. 1.9e-255; Matches 773; Conservative 144; Mismatches 238; Indels 14
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                                                                                       GIWVVFKIPTINGYATLGNLELVEEGPLSGETLERAQQOEQQWQDKWARKRGASEKAYYA
      YLGDTIEKONFPNKTMDNGASLIYETFKFASFITDFOFRETQDKILLSMGDFSSGQEVYID
                                                                       LLPDVLPVNSCQGIDRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEIDLNENT
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                      TLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNLRLFVT
                           599 ISGTRIYSINVNKTMNKGDDLFFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGBVYVD
                                                                  KPEL I PVNATPRAREDLDVAKKAVNGLPTSKKDALQTSVTOYQVNQAANLVRCLSDRLYP
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                                                                                                                                                                                                                                                                                                                                      B-18746; pMYC1638; Colorado potato
                                                                                                                                                                                                                                                                                                                           B.thuringiensis PS50C Coleopteran-active toxin.
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                                                                                                                           The toxin can be used to control coleopteran pests, esp. soil-inhabiting coleoptera. The C-terminal Glu residue corresponds to a CAG (Gln) codon. The protein is obtained from a new isolate of Bacillus thuriengiensis
                                                               and
                                                                                                                                                                                                                                                                                                                                                                          SSIPSPAVSGHEVILLAVYAQAVNLHILILADASIFGBEWGFTPGBISRFYNRQVQLTAB
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                                                               New Bacillus thuringiensis isolate - used for preparing to transformed hosts for controlling coleoptera insect pests
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66.1%; Score 3995; DB 2;
Best Local Similarity 66.0%; Pred. No. 1.2e-254;
Matches 771; Conservative 145; Mismatches 239;
                                                                                                       Claim 12; Page 18-20; 33pp; English
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Best Local Similarity
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(Updated on 24-OCT-2003 to standardise OS field)
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                                         Length 1157;
                                                               Indels
                                         Match 66.1%; Score 3994; DB 2; Local Similarity 66.0%; Pred. No. 1.4e-254; e8 771; Conservative 144; Mismatches 240;
 correct PF field.)
                      Sequence 1157 AA;
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Best Local S:
Matches 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding the insecticidal toxin can be cloned into baculo viruses ar transferred to other host microbes, preferably B. coli NM522(pMYC 2320) NRAL B-18769, to control acaride peste, or to plants which become resistant to the acaricide peste. Specifically, the two-spotted spider mite (Tetranychus urticae) is controlled. (Updated on 25-MAR-2003 to
RLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
                                                      GIWVGFKITDPEGYATLGNLELVEEGPLSGDALERLQREEQQWKIQWTRRREFIDRRYMT
                                                                                                                                                                                     RIQQAWNLYDQRNAIPHGDFRNGLSNWATFGVEVQQINHTSVLVIFNWDEQVSQQFTVQ
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                                           LLPDVLPVNSCGGI DRCSEQQYVDANLALENNGENGNMSSDSHAPSFHIDTGEI DLMBNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spider mite - utilising
into microbe hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus thuringiensis serovar kumamotoensis; (isolate PS50C)
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biological control agent; transgenic plant; crop improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis crystal protein PS50C
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91US-00759248.
91US-00768141.
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13-SEP-1991;
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25-MAR-2003
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                                                              PNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSADQTSYITKTVEFT 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain of Bacillus thuringiensis serovar japonensis - producing toxin
PNORYVIRVTARKEGVGVGYVSIRDGGNQSETLIFSASDYDTNGVYNDQTGYITKTVTFI
                           RLQQAWNLYDLRNAI PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQ
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thuringiensis; virus; insect; FBRM BP-3465.
                                                                                                    PSTEQVWIDMSETEGVFNIESVELVLEEE 1167
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PYTDQMWIEISETEGTFYIESVELIVDVE 1157
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751. .766
//note= "amino acids 751-766 are not given in the
specification and so have been decoded from AAQ58975"
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                                                           1114 NICODDIGVLSADQISYITKIVEFIPSTEQVWIDMSETE 1152
                                                                                           1107 NICDDDTGVLSTDQTSYITKTVEFTPSTEQVWIDMSETE 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.thuringiensis serovar Japonensis insecticidal
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                                                                                                                                                                                                                                                                           AAR51692 standard; protein; 1149
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N-PSDB; AAQS8975.
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S--ISSARYIRHWAGHQISYHRIPSDNIIKQMYGTNQNLHSTSTPDFTNYDIYKTLSKDA 414
                                           DLAN-----YAQVYGVPYASFTLLDK--NTGSGSVGGFTYSKPHTTMQVCTQNYNTID- 470
                                                                                                                                                                                                                                                                                                                                              Pesticidal; spraying; dusting; broadcasting; seed coating; insect pest; Colorado potato beetle; western corn rootworm; southern corn rootworm; insect target range; endotoxin; Cryl218.
                                                                                                                                                                         ADLINAVESDKITQIPVVKVSDLAPSITGGPNNTVVSGPGFTGGGIIKVIRNG-VIISHM
                                                                                                                                                                                                                                  571 RVKISDINKEYSNRIRYASANNTEPYINPSERNKS-HAQKTYMRGRALTYNKFNYATL-
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                                                                                                                 DIIAGTRDSELELPPETSDQPNYESYSHRLCHITSIPATGSTT----GLVPVPSWTHRS
                                                                                                                                                          ADVINITVYSDKITQIPVVKAHTL---VSG---TTVIKGPGFTGGNILKRTSSGPLAYTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm or for invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a Bacillus thuringiensis wild-type Cry1218
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                                                                                                                                                                                                                                                                                                                                              New isolated pesticidal polypeptide useful for impacting insect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 178; Mismatches 284; Indels 119;
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                                                                                                                                                                                                                                                                            Sime
                                                                                                                                                                                                                                                                            Kabn TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.0%; Score 3263.5; DB 5; 53.4%; Pred. No. 2.6e-206;
Bacillus thuringiensis Cryl218-2 protein sequence
                                                                                                                                                                                                                                                                          Flannagan RD,
                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 103-105; 176pp; English
                                                                                                                                                                                                                                              (DUPO ) DU PONT DE NEMOURS & CO B I.
                                                                                                                                                                                                  24-OCT-2000; 2000US-0242838P.
23-OCT-2001; 2001US-00032717.
                                                                                                                                                                         24-OCT-2001; 2001WO-US045468
                                                                                                                                                                                                                                                                          Feng X,
                                                                                                                                                                                                                                                                                                                                                              Colorado potato beetle.
                                                                                   Bacillus thuringiensis
                                                                                                                                                                                                                                                                          Duck NB,
                                                                                                                                                                                                                                                                                                    2002-519178/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
667; Conserv
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                                                                                                                WO200234774-A2
                                                                                                                                            02-MAY-2002
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Best Local S:
Matches 667
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---TLKYNPVSK
                                                 DIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPATCATT----GLVPVPSWTHRS
                                                                                                   518 ADVINIVYSDKITQIPVVKAHTLVSGTTVIKGPGFTGGNILKRISS----GPLAYTSVSV
                                                                                                                                                                        574 KSPLSQRYRARIRYASTTNLRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAF
                                   ------EIPPE--NEPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRS
                                                                                                                                                                                                                                                                                                         KDALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKBAKRLVQARNLLQDTGFNRI
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 415 VLLDIVYPGYTYIFFGMPEVEFFWVNQLNNTRK--
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new pesticidal polypeptide. The invention is useful for impacting an insect pest by applying the the molecules of the invention to the environment of the insect pest by spraying, dusting, broadcasting, or seed coating, where the insect pest is selected from Colorado potato beetle, western corn rootworm or southern corn rootworm. The invention is also useful for increasing insect target range and for producing transgenic microorganisms and plants that express the pesticidal polypeptide. The invention is also useful for producing transformed plants and in transforming any organism to produce the pesticidal polypeptide of the invention. The present amino acid sequence represents a Bacillus thuringiensis wild-type Cry1218 endotoxin protein
                                                                                                                                                                                                                                                                                                                                e.g.
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                                                                                                                                                                                                                                                                                                                            New isolated pesticidal polypeptide useful for impacting insect Colorado potato beetle.
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                                                                                                                                                                                                                                             Feng X,
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                     thuringiensis.
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                                                                                                                                                                                                                                             Abad AR, Duck NB,
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411 SNGAVLLDIVYPGYTYTFFGMPETEFFMVNQLNNTRKT--LTY-KP-ASKDIIDRTRDSE
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SLGADLAN----YYAQVYGVPYASPTLLDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTI
                                                                                                                                                                                                                                                                                                                                                                              TVGADS-----PASGGEVYV-DKPELIPVNATFBAEEDLDVAKKAVNGLFTSKKDAL
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ESVELIVDVB 1169
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Synthetic.
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The DNA encoding this sequence was isolated from the Bacillus thuringiensis strain kumanchoensis. Insects in the family Scarabaeidae constitute a serious pest control problem, especially when destructive larval stage insects infest high value turf found in golf courses.

I playing fields and lawns. The larvae of many species also attack grains, tuberous crops, and ornamentals. The larvae are known as white grubs, or chafer grubs, and ornamentals. The larvae are known as white grubs, or chafer grubs, and ornamentals. The larvae are known as white grubs or chafer grubs, and ornamentals. The larvae are known as white soil these larvae and adults have developed resistance to chemical insecticides such as the organochlorines and DDT. These toxin sequences, and intact cells that are capable of expressing these proteins, can be used to control many pests of the family scarabaeidae, such as species of cyclocephala, and Popillia. The toxins are active against larvae (present in soil) and against adults. (Updated on 16-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BTPIS-SSTVOTGIGIVGOVIGALGVPFAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVB 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding B.thuringiensis toxin active against scarab(s) - also related toxin and transformed microbes, effective against adult pests and their larvae.
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                                                                                                                                                                                                                                                                                                                 Michaels TE;
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                                                                                                                                     91US-00808316.
92US-00828430.
93US-00014941.
                                                                                 94US-00315468
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                                                                                 30-SEP-1994;
                                                                                                                                           16-DEC-1991;
                                                                                                                                                                         30-JAN-1992;
01-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                            PHIDTGRIDLNENTGIWVVPKIPTTNGYATLGNLELVBEGPLSGBTLERAQQQEQQWQDK 944
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                                                                                                               360 -PPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTTRATINPGVDGTNR----IBST
                                                                                              ENBPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI
                                                                                                                                                                                RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAPS
                                GADLANYYAQVYGVPYASFIL--LDKNTGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPP
                                                                                                                                                               PVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSGRYRARIRYASTTN
                                                                                                                                                                                                                               593 IRLEVIISGTRIYSINVNKTMNKGDDLIFNTF---DLATIG---TAFTFSNYSDSLTVGA
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                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing more transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured cells of the transgenic plants and used in insecticide compositions against lepidopteran insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. Another B.thuringiensis derived crystal protein, especially CryMb- or Cry1B-type protein), and used to transform B.thuringiensis, which crystales other insecticidal toxins. Such strains are useful against a variety of insect pests, or insects where insect resistance development is prevented or delayed. (Note: this sequence is not given in the insection).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ETPISS-STVQTGIGIVGQVLGALGVPPAGQIASFYSPIVGQLWPSSTVSVWEMIMKQVR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                               New Bacillus thuringlensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                                                                                               (PLBZ ) PLANT GENETIC SYSTEMS NV
                                                                                                                                                                                                                                                                                                                 Example; Page; 40pp; English.
                                                                 98WO-EP004033
                                                                                                97US-00884389
                                                                                                                                                                 Van Rie J;
                                                                                                                                                                                                WPI; 1999-105666/09
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grandiosella.

                                                                 25-JUN-1998;
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 WO9900407-A2
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Amino acid sequence of Bacillus thuringiensis Cry9C mutant
Cry9C; crystal protein; toxic; mutant; insecticide; transgenic plant; transgenic seed; lepidoptera.
                                                                                           AAW84584 standard; protein; 1157 AA
                                                                                                                                               07-JUN-1999 (first entry)
                                                                                                                                                                                                                                      Bacillus thuringiensis.
Synthetic.
                                                                                                                                                                                                                                                                               WO9900407-A2
                                                                                                                     AAW84584;
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                                                                               QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREWTLLVLDLVALPPNYDTRTYPIETTA 299
                                                                                                                                                                                        QLTREVYTDPIVFNRETSGGFCRRWSLNSDISFSEVBSAVIRSPHLFDILSBIBFYTTRA 359
                                                                                                                                                                                                                                          GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
                                                                    DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF
                                                                                                                      VAKIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
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1065 PNWNSQVSQQFTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTBTLTFNICDDDTGVLS 1124
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                                                                                                                                                           DSPASGGEVYVDKPELIPVNATPEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAA
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                  LRLFVTISGTRIYSINVNKTMAKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA
417 GADLANYYAQVYGVPYASPTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
                                                                      ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cry9C; crystal protein; toxic; mutant; insecticide; insect; transgenic plant; transgenic seed; lepidoptera.
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                                                                                                                                                                                                                New Bacillus thuringiensis Cry9C crystal proteins with improved toxicity - useful for producing transgenic plants in controlling pest insects, especially Ostrinia nubilalis, Heliothis virescens and Diatraea
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Matches 620; Conservative 195; Mismatches 326; Indels
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07-JAN-1999
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414 AVDFRSALIGIYGVNRASFVPGGLFNGTTSPANGG----

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This is the amino acid sequence of a Cry9C (crystal) mutant protein which is toxic to an insect species. It is modified in the method of the invention in an attempt to improve its toxicity. The improved proteins are useful for producing transgenic plants and seeds in controlling insects feeding on a plant. The transgenic plants are also useful for producing more transgenic plants with similar characteristics, or for introducing the improved cry9C gene (including fragments) into the same plant variety or related plant species. The Cry9C protein can be obtained from cultured cells of the transgenic plants and used in insecticide compositions against lepidopteran insect control protein (e.g. telliothis virescens and Diatraea grandiosella. The cry9C gene can be expressed in combination with another insect control protein (e.g. Another B. thuringiensis derived crystal protein, especially Cry1Ab- or Cry1B-type protein), and used to transform B. thuringiensis, which crysches other insecticidal toxins. Such strains are useful against a variety of insect pests, or insects where insect resistance development is speciation, but is generated using the information provided by the
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                                                                                       (PLBZ ) PLANT GENETIC SYSTEMS NV.
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Sequence 1157 AA;

OLTREVYTOPIVENRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSBIEFYTTRA 359 QXSDXCVKWYNTGLDXLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTA 299 GLPLANTEYLEYWYGHSIKYKNTWASSALERNYGTITSNKIKY---YDLANKDIFQVRSL 416 - PPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITHTRATINPGVDGTNR----IEST 413 GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP 474 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALBLDP VAXIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA Gaps = = = 42; Length 1157; Query Match 51.7%; Score 3126; DB 2; Length 11: Best Local Similarity 52.3%; Pred. No. 2.9e-197; Matches 619; Conservative 195; Mismatches 327; Indels 120 121 180 181 241 301 240 300 360 8 셤 ઠે 윱 셤 윱 È 셤 8 & 셤 δ 8 ઠે

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                               LRLPVTISGTRIYSINVNKTMNKGDDLTFNTP---DLATIG---TAFTFSNYSDSLTVGA
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SUMMAKIBS	ΩI	US-10-089-678-1	US-10-032-717-4	US-10-414-637-4	US-10-606-320-4	US-10-032-717-2	US-10-414-637-2	US-10-606-320-2	US-10-099-285-72	US-10-428-961-28	US-10-614-524-6	US-10-099-285-74	US-10-099-285-76	US-09-988-462-7	US-10-428-961-63	US-09-826-660-23
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ALIGNMENTS

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Sequence 1, Application US/10089678

Sequence 1, Application US/10089678

Publication No. US20030017967A1

GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD
FILE REPERENCE: Q68021

CURRENT APPLICATION NUMBER: US/10/089,678

CURRENT FILING DATE: 2002-05-02

FRIOR PELING DATE: 2000-236140

FRIOR PLING DATE: 2000-03

FRIOR FILING DATE: 2000-03

FRIOR FILING DATE: 2000-08-03

FRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PATENTIN Version 3.1

SEQ ID NOS: 3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1167; Conservative 0; Mismatches 0; Indels 0;
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US-10-089-678-1
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1021 QQAWNLYDLRNAI PNGDFRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPN
                                                                                                                                                                      ELI PONATPEAERDLDVAKKAVNGLPTSKKDALQTSVTDYQVNQAANLVECLSDELYPNE
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                               YSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTAQ
                                                               LTREVYTDPIVPNRETSGGFCRRWSLNSDISPSBVBSAVIRSPHLFDILSEIBFYTTRAG
                                                                                              LPLNNTEYLEYWYGHSIKYKNTNASSALBRNYGTITSNKIKYYDLANKDIFQVRSLGADL
                                                                                                       LPLINITEYLEYWYGHSI KYKNTNASSALERNYGTI TSNKI KYYDLANKDI FOVRSLGADL
                                                                                                                              ANYYAQVYGVPYASPTLLDKATGSGSVGGPTYSKPHTTMQVCTQNYNTIDBIPPENBPLS
                                                                                                                                      ANYYAQVYGVPYASFILLDKATGSGSVGGFTYSKPHTIMQVCTQNYATIDEIPPENBPLS
                                                                                                                                                              RGYSHRLSHITSYSPSKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAHTL
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RESULT 2 US-10-032-717-4 ; Sequence 4, Application US/10032717

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GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Micholas B. Duck
APPLICANT: Micholas B. Duck
APPLICANT: Xiang Peng
APPLICANT: Tonaid D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn B. Sims
ITITLE OF INVENTION: Genes Bncoding No. US20020151709Alel Proteins With
ITITLE OF INVENTION: Pesticidal Activity Against Coleopterans
PILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/032,717
CURRENT PILING DATE: 2001-10-23
PRIOR PLLICATION NUMBER: 60/242,838
PRIOR PLLICAN DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastsEQ for Windows Version 4.0
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Best Local Similarity 53.4%; Pred. No. 3e-258;
Matches 667; Conservative 178; Mismatches 284; Indels 119;
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APPLICANT: Andre R. Abad
APPLICANT: Andre R. Duck
APPLICANT: Xiang Feng
APPLICANT: Xiang Feng
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lyun B. Sime
TITLE OF INVENTION: Genes Encoding No. US20030177528Alel Proteins With
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 15718/237005
CURRENT APPLICATION NUMBER: US/10/414, 637
CURRENT PLILNG DATE: 2003-04-16
PRIOR FILING DATE: 2001-10-23
PRIOR PLILING DATE: 2001-10-23
PRIOR PLILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
STOWNER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 2, Application US/10032717
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Nicholas B. Duck
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Parm B. Sims
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: Pesticidal Activity Against Coleopterans
TITLE OF INVENTION: US STANDES
THE REFERENCE 1957105
CURRENT APPLICATION UNDERS: 105/10/032,717
CURRENT FILING DATE: 2001-10-23
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is Sequence 4, Application US/10606320
is GENERAL INFORMATION:
is GENERAL INFORMATION:
is APPLICANT: Andre R. Abad
is APPLICANT: Renald D. Flannagan
is APPLICANT: Abed Hermann
is APPLICANT: Theedore W. Kahn
is APPLICANT: Billy Fred McCutchen
is APPLICANT: James F.W. Presnail
is APPLICANT: James F.W. Presnail
is APPLICANT: James F.W. Wong
is TITLE OF INVENTION: Genes Encoding Proteins With Pesticidal
iTITLE OF INVENTION: WOWBER: 60/320
iCURRENT FILING DATE: 2003-06-25
iPRIOR FILING DATE: 2002-06-25
iPRIOR FILING DATE: 2003-04-04
iNUMBER OF SEQ ID NOS: 134
iLEANTH: JAMES FREENCE FOR WINDOW VERSION 4.0
iLEANTH: JAMES
                                     TETLTFNICDDDT-GVLSA---
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US-10-606-320-4
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1101 TLTPSASDYDTNGMYNTQVSNTNGYNTNNAYNTQASSTNGYNANNMYNTQASNTNGYNTN 1160
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APPLICANT: Xiang Peng
APPLICANT: Xiang Peng
APPLICANT: Xiang Peng
APPLICANT: Xiang Peng
APPLICANT: Annual D. Plannagan
APPLICANT: Theodore W. Kahn
APPLICANT: Theodore W. Kahn
APPLICANT: Lynn E. Sims
TITLE OF INVERTION: Genes Encoding No. US20030177528Alel Proteins With
TITLE OF INVERTION: Pesticidal Activity Against Coleopterans
FILE REFERENCE: 35718/237005
CURRENT APPLICATION NUMBER: US/10/414,637
CURRENT PILING DATE: 2003-04-16
PRIOR PLLING DATE: 2001-10-23
PRIOR PLLING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 48
SOFTMARE: FastSEQ for Windows Version 4.0
SSEQ ID NO 2
FENNMENT: 1704
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                                930 TLERAQQQBQQWQDFWARFRGASBKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQN
                                                                                                      .050 DVNVQQLSDTSVLVIPNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTB
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53.7%; Score 3246.5; DB 14; Length 1206;
Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Mismatches 290; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10414637; Publication No. US20030177528A1; GENERAL INFORMATION: APPLICANT: Andre R. Abad; APPLICANT: Nicholas B. Duck
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                                                                                                                                                                         Query Match 53.7%; Score 3246.5; DB 13; Length 1206; Best Local Similarity 53.4%; Pred. No. 7.5e-257; Matches 665; Conservative 172; Mismatches 290; Indels 119;
PRIOR APPLICATION NUMBER: 60/242,838
PRIOR FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2
LENGTH: 1206
                                                                                                                    / ORCANISM: Bacillus thuringiensis
US-10-032-717-2
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                                  QLTREVYTOPIVPNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIEFYTTRA 359
                                            S--ISSARYIRHWAGHQISYHRVSRGSNLQOMYGTNQNLHSTSTFDFTNYDIYKTLSKDA 414
                                                                                                      DLAN-----YYAQVYGVPYASFTLLDK--NTGSGSVGGFTYSKPHTTMQVCTQNYNTID- 470
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                                                                                                                     415 VLLDIVYPGYTYIPPGMPEVBPRVNQLNNTRK--------TLKYNPVSK 456
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Best Local Similarity 53.4%; Pred. No. 7.5e-257;
Matches 665; Conservative 172; Migmatches 290; Indels 119;
                                                                   APPLICANT: Ronald D. Flannagan
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Rafael Herrmann
APPLICANT: Albert L. Lu
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James F.H. Wong
CURRENT PILING DATE: 2003-06-25
FRIOR PILING DATE: 2003-06-25
FRIOR APPLICATION NUMBER: 60/460, 787
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US-10-606-320-2
ion No. US20040091505A1 INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 51.3%; Score 3100.5; DB 14; Lengt
Best Local Similarity 52.0%; Pred. No. 6.9e-245;
Matches 615; Conservative. 196; Mismatches 330; Indels
                                                                                                                                                                     ATTORNY DALES TANGER TO SERVICE TO SERVICE TO SERVICE 
                      APPLICATION NUMBER: 09/002,285
PILING DATE: «Unknown»
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
APPLICATION NUMBER: US 08/674,002
PILING DATE: 1-JUL-1996
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SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-099-285-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
     PRIOR APPLICATION DATA:
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ALEKAGKYRVRLRYATDADIVLHVNDA-----QIQMPKTWNPGEDLTSKTPKVADALTTL 626
                                                                                 ---TFSNYSDSLTVGADSPAS-GGEVYVDKFELIPVNATFEAREDLDVAKKAVNGLFTSK 689
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                                                                                                                NGENGWIGSIGIEVARGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKL
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Publication No. US20030105319A1
GENERAL INFORMATION:
MICKET, CATOL
MARYA, Kenneth E.
WALZ, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Saliwanchik, iloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099, 285
FILING DATE: 15-MAR-2002
CLASSIFICATION: <Unknown>
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US-10-099-285-72
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SLSISGRDAVQTALTVVGRILGALGVPFSGQIVSFYQFLLNTLMPVNDTAIWEAFMRQVE 120
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                                                                                                                                                                                                593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT----AFTFSNYSDSLTVGAD
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                                                         DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLKNRNDTRARSVVVTQYIALBLDP
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Sequence 28, Application Wo. 10320337111A1

GENERAL INFORMATION:

APPLICANT: Bunn, James A.

APPLICANT: Chu, Chih Rei

APPLICANT: Chu, Chih Rei

APPLICANT: Chu, Chih Rei

APPLICANT: Chu, Chih Rei

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringlensis Delta-Endotoxin

TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringlensis Lepidopteran-Active Bacillus thuringlensis Lepidopteran-Active Bacil
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   SST SSEYFIDELIFICATION STREAMENT STRENGLOWN TO COMPAN 698
                                                                                                                                                                                                   HHKVHLVKNVPDNLVSDTYSDGSCSGINRCDEQHQVDMQLDAEHHPMDCCEAAQTHEFSS 874
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                                                                                                                           HRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFSF
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952 SEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPEIPGMNYT 1011
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                                                                                                   ELYPNEKRMGMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAEGDVLFKD 772
                                                                                                                                                                                                                                  RSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPIGSSQDLEIKKIRHRANQIV 832
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595 LEVIISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGE
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ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STREE: Florida
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TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-MAR-2002
CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 09/002,285
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Narva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
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COMPUTER READABLE FORM:
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                                                                                                                                                                       APPLICANT: Arnaut, Greta
APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Boets, Annemie
APPLICANT: Dammes, Nicole
APPLICANT: Mathieu, Eva
APPLICANT: Wanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
CURRENT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
APPLICANT: Vanneste, Stijn
CURRENT: Vanneste, Stijn
APPLICANT: NIWHER: US/09/10/614,524
CURRENT FILING DATE: 2003-07-08
PRIOR APPLICATION NUMBER: US/09/739,243
PRIOR APPLICANTION NUMBER: 60/173387
PRIOR PLING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SECTION OF SECTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VAKIPSFAI----SCOEVPLLSVYAQAANLHILLIRDASIFGAEWGFTFGEISTFYDRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.7%; Score 2884.5; DB 15; Lengtl Best Local Similarity 49.1%; Pred. No. 3.8e-227; Matches 578; Conservative 200; Mismatches 365; Indels
                                                                                                   Sequence 6, Application US/10614524
Publication No. US20040016020A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-614-524-6
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NWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSA 1125
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929 GRKRABTDRIYQDAKQAINHLFVDYQDQQLSPEVGMADIIDAQMLIASISDVYSDAVLQI
                                                                                                                                                                      HHKVHLVKNVPDNLVSDTYSDGSCSGINRCERQHQVDVQLDABDHPKDCCBAAQTHBF8S
                                                                                                                                                                                                                                           869 YIHTGDIAMASVDQGIWVVLQVRTTDGYATIGALELVEVGPLSGESLEREQRDNAKWNEEV
                                                                          GDVLPKDRSLRLTSARRIDTBTY PTYLYQQIDBSLLKPYTRYKLKGFIGSSQDLBIKLIR
                                                                                                                                               HRANOI VKUVPDNILLPDVLPVNSCGGI DRCSBQQYVDANI.ALENNGENGNMSSDSHAPSP
                                                                                                                                                                                                                                                                                               946 ARKRGASEKAYYAAKQAIDRLFADYQDQKINSGVEMSDMLAAQNIVQSIPYVYNDALPBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1109 NDNSYITKELVFYPKTEHMWEVSFTEGTFYIDSIBFIETGE 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 76, Application US/10099285;
Publication No. US20030105319A1
GENERAL INFORMATION:
Micker, Carol
Micker, Carol
Marva, Kenneth B.
Walz, Michelle
Stockhoff, Brian
Muller-Cohn, Judy
TITLE OP INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUWRRY: USA
ZIP: 32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/099,285
FILING DATE: 15-Mar-2002
CLASSIFICATION: «UDKNOWD»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: «Unknown»
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REPERENCE/DOCKET NUMBER: MA-701C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIBPYTTRAGLPLANYTEYLEYWYGHSIKYKNTNASSALERNYGTITSNKIKYYDLANKDI 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POVRSIGADLANYYAQVYGVPYASPILLDKNYGSGSVGGPTYSKPHTTMQVCTQNYNTID 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOIPVVKAHTLVSGTTVIKGPGPTGGNILKRTSSGPLAYTSVSVKSPLSORYRARIRYAS 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTN--LRLFVTISGTRIYSINVNXTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGAD 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 BLFGNPETFISSSTVQTGIGIVGQVLGALGVPPAGQIASPYSFIVGQLWPSSTVSVWEMI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
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                                                                                                                                                                                                                                                                                                                                                                                       Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                                            47;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
46.7%; Score 2825.5; DB 14; Lengt!
Best Local Similarity 48.6%; Pred. No. 2.6e-222;
Matches 574; Conservative 197; Mismatches 364; Indels
                                                                                      NAME: Sandere, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
TELECOMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 375-8100
TELEPHONE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 08/886,615
FILING DATE: 1.-UL-1997
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1.-UL-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
                                                                                                                                                                                                                                             LENGTH: 1150 amino acids
                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       US-10-099-285-74
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名 ò 셤 ઠે

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PADYQDQKINSGVEMSDMIAAQNIVQSIPYVYNDALPEIPGMNYTSFTELTNRLQQAWNL 1026
                                                                                                                                                                                                       VTARKEGVGDGYVIIRDGANQTETLTFNICDDDTGVLSADQTSYITKTVBFTPSTEQVWI 1146
                                                                                                                                                                                                                                                                      1054 VTAEKVGGGGGTYVTIRDGAHHTETLTFNACDYDINGTYVTDNTYLTKEVIFYSHTEHDWV 1113
                                                                               PTTNGYATLGNLELVEEGPLSGETLERAQQQEQQWQDKMARKRGASEKAYYAAKQAIDRL
 SCGGIDRCSEQOYVDANLALENNGE-NGNMSSDSHAPSFHIDTGEIDLNENTGIWVVFKI
                  YDLRNAI PNGDPRNGLSDWNATSDVNVQQLSDTSVLVI PNWNSQVSQQFTVQPNYRYVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INVENTION: SYNTHETIC DNA SEQUENCE HAVING BINSECTICIDAL ACTIVITY IN MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-00. US20030046726A1-2001
CLASSIFICATION: «Unchown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/971,027
FILING DATE: 25-SEP-1992
FILING DATE: 04-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSER: Syngenta Biotechnology, Inc.
STREET: 3054 COTMWallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFREENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                     1114 EVNETEGAPHIDSIEPVETEK 1134
                                                                                                                                                                                                                                                                                                                      DMSETEGVFNIESVELVLEER 1167
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Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Bllis J.
Launis, Karen L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09988462
Publication No. US20030046726A1
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 94
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SKNASSPARYGNLPVPAWTHRSADVTNTVYSDKITQIPVVKAHTLVSGTTVIKG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTNIRLFVTISGTRIYSINV 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 NKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEVYVDKFELIPVNATF 669
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|||||:||:||||||||||||||
YPTYIYQKVDASELKPYTRYRSDGFVKSSQDLEIDLIHHHKVHLVKNVPDNLVSDTYPDD 813
                                                                                                                                                                                                                                                                                                                                                                                                                    LILIRDASI PGAEWGPTPGEISTPYDROV-TRTAOYSDYCVKWYNTGLDXLKGTNAASWLK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YHQPRREMTLLVLDLVALPPNYDTRTYPIBTTAQLTREVYTDPIVFNRBTSGGF----CR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWSLNSDISPSEVESAVIRSPHLPDILSEIBPYTTRAGLPLNNTEYLEYWGHSI--KYK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WINASSALERNYGTITSNKIKYYDLANKDIPQVRS---LGADLANYYAQVYGVPYASFTL 437
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                                                                                                                                                                                                                                                                                                                                     93 SFYSFIVGQLWPSSTVSVWEMIMKQVBDLIDQKITDSVRKTALAGLQGLGDGLDVYQKSL 152
                                                                                                                                                                                                                                                                                                                                                                                                KNWLENRNDTRARSVVVTQYIALELDFVAKIPSPAISGQ-----EVPLLSVYAQAANLHL 207
                                                                                                                                                                                                                                                                                        4 NPNINECIPYNCLSNPEVEVLGGERGNVRT----GLÓTGIDIVAVVGALGGPVGGILT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RABEDLDVAKKAVNGLPTSKKDALQTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVK
                                                                                                                                                                                                                                                                        NWNYKDYLRMSEGENPEL-----PGNPETPISSSTVQTGIGIVGQVLGALGVPPAGQIA
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                       Length 1134;
                                                                                                                                                                                                       Query Match

44.8%; Score 2710; DB 14; Length Best Local Similarity 48.1%; Pred. No. 7.9e-213;
Matches 559; Conservative 195; Mismatches 345; Indels
                                                                               TYPE: amino acide

TYPE: amino acide

STRANDEDNESS: single

TOPOLGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 76:

US-10-099-285-76
                  TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
 FELECOMMUNICATION INFORMATION
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1134 amino acids
                                              INFORMATION FOR SEQ ID NO: 76:
                                 TELEFAX:
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APPLICANT: Baum, James A.
APPLICANT: Baum, James A.
APPLICANT: Chu, Chih-Rei
APPLICANT: Chu, Chih-Rei
APPLICANT: Donovan, William P.
APPLICANT: Gilmer, Amy J.
APPLICANT: Gilmer, Mark J.
TITLE OF INVENTION: Lepidopteran-Active Bacillus thuringiensis Delta-Endotoxin
TITLE OF INVENTION: Polymolectides, Compositions, and Methods of Use (Amended)
FILE REFERENCE: MECO201-1
CURRENT PILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/661,322
PRIOR APPLICATION NUMBER: 60/153,995
PRIOR FILING DATE: 2000-09-13
                                                                                                                                                                                                                                                                  1021 QQAWNLYDLRNAIPWGDFRWGLSDWNATSDVNVQQLSDTSVLVIPWWNSQVSQQFTVQPN 1080
                                                                                                                                                                                                                                                                                                                                                              1051 CGYLLRYTAYKEGYGEGCVTIHEIENNTDELKPKNREBEEVYPTDTGTCNDYTAHQGTAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                       | |: | | :: | | 1.10 | 11.11 | 1.12 | | 1.13 | 1.14 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15 | 1.15
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167 NAMPLPAIRNQEVPLIMVYAQAANIHLILILIABASLFGSEFGLTSQEIQRYYERQVBKTRB 226
                                                                        813 VESPIGRCGEPNRCA--PHPEWNPDLDCSCRDGERCALHSHHPSLDIDVGCTDLHENLGV
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                                               WVVPKI PTTNGYATLÆNLELVEGPLSGETLERAQQQEQQWQDIOMARKRGASEKAYYAAK
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40.7%; Score 2457; DB 15; Length 1227;
Best Local Similarity 42.8%; Pred. No. 5.4e-192;
Matches 541; Conservative 197; Mismatches 392; Indels 134;
                                                                                                                                                                                                                                                                                                                                     1081 YRYVLRVTARKEGVGDGYVIIRDGANQTETLTF-------
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; Publication No. US20030237111A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 63
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 LVLDLVALPPNYDTRTYPIETTAQLTREVYTDPIVFNRRTSGGFCRRWSLNSDISFSEVE 336
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                                                                                                                                                                                                                                                          Query Match
41.7%; Score 2519.5; DB 10; Length 1207;
Best Local Similarity 44.3%; Pred. No. 3.9e-197;
Matches 548; Conservative 178; Mismatches 372; Indels 139; Gaps
                                                                                                                                                                                            7.
                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                      TELEPAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 amino acids
    (919) 541-8587
                                                                                                                       TYPE: amino acid
                                                                                                                                        TOPOLOGY: linear
    TELEPHONE:
                                                                                                                                                                                                                US-09-988-462-7
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Sequence 23, Application US/09826660
Patent No. US20010026940A1
GENERAL INFORMATION:
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48 DPFVSASTVQTGINIAGRILGVLGVPFAGQIASFYSFLVGELWPRGR-DPWBIFLEHVBO 106
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APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth B.
TILE REPERENCE: MA-714XC2D1
CURRENT PAPLICATION NUMBER: US/09/826,660
CURRENT PILING DATE: 2001-04-05
FRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
PRIOR PLING DATE: 1998-10-23
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1997-11-12
PRIOR PLING DATE: 1998-03-02
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 23
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40.6%; Score 2454.5; DB 9; Length 1186;
Best Local Similarity 43.1%; Pred. No. 8.3e-192;
Matches 536; Conservative 191; Mismatches 382; Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Toxin encoded by synthetic B.t. gene US-09-826-660-23
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FVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGTAFTFSNYSDSLTVGADSFASGGEV 655 : : : : STATE :	YVDKPELIPVNATPRAEBDLDVAKKANNGLFTSKKD-ALCTSVTDYQVNQAANLVBCLSD 714	ELYPNEKRMINDAVKEARRIVQARNILQDIGFNRINGENGWIGSTGIEVAEGDVIFKD 772 : : : : : : : : BPCLDEKKELSEKVKHARRISDERNILQDPNFRGINRQLDRGWRGSTDITIQGGDDVFKE 748	RSIRLTSAREIDTETYPTYLYQQIDESLIKPYTRYKLKGFIGSSQDLEIKLIRHRANQIV 832 	KNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALERNGENGNMSSDSHAFSFHIDTGEI 892	DINENTGIWUVEKI PITNGYATLANLELVEEGPLSGEFLERAQQOBQQNQDEMARKRGAS 952 : : : : : : : : :	EKAYYAAKQAIDRLFADYQDQKLANSGVEMSDWLAAQNLVQSIPYYYNDALPEIPGANYTS 1012 	PTELTNRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNV-QQLSDTSVLVIPNWNSQV 1071 	SQOFTVQPNYRXVLRVTARKEGVGDGYVIIRDGANQTETLIFNICDD 1118 :	DDGV	1130YITKIVBFTPSTEQVWIDMSETEGVENIBSVELVLEBE 1167 - : : : :	
596 FVT	656 YVD : 629 HPD	715 ELY 689 BPC	773 RSE. 749 NYV	833 XXVV 806 VXV	893 DLN 843 DLN	953 EKA	1013 FTE 963 FEE	1072 SQQ : 1023 SQE	1119 DTG 1083 YTA	1130	
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Search completed: June 21, 2004, 13:45:40 Job time : 70 secs

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Sequence 30, Appli
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Sequence 7, Appli
Sequence 72, Appli
Sequence 72, Appli
Sequence 74, Appli
Sequence 74, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 76, Appli
                                                                          June 21, 2004, 13:36:05; Search time 23 Seconds (without alignments) 2619.457 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  - protein search, using sw model
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Perfect score:
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APPLICANT: Payre, Jewel M.
APPLICANT: Bagley, Angela L.
TITLE OF INVENTION: No. 5262188el Bacillus thuringiensis Isolates for TITLE OF INVENTION: Controlling Acarides
TITLE OF INVENTION: Controlling Acarides
CORRESPONDENCE ADDRESS:
ADDRESSES: David R. Saliwanchik
                                                                                              Sequence 7, A Sequence 7, A Sequence 7, A Sequence 7, A Sequence 8, A Sequence 9, A Sequence 63, Sequence 23, Sequence 14, A S
Sequence Seq
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
SOOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/876,280
PILING DATE: 1920430
CLASSIPICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Saliwanchik, David R.
REFERENCE/DOCKET NUMBER: M/S 104
TELLEPHONE: 904-375-8100
TELLEPHONE: 904-375-5100
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
'PWATH: 1157 amino acids
                                                                US-07-951-715A-7
US-08-459-595A-7
US-08-459-595A-7
US-08-459-5944-7
US-09-547-45-7
US-09-547-42-7
US-09-547-42-7
US-09-547-43-8
US-09-661-803-9
US-09-661-322A-63
US-09-661-322A-63
US-09-826-660-23
US-09-826-660-23
US-09-826-660-23
US-09-826-660-23
US-09-61-32A-38
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US-07-876-280-30
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STRAIN: kumamotoensis
INDIVIDUAL ISOLATE: PS50C
IMMEDIATE SOURCE:
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; Sequence 30, Application US/07876280

; Patent No. 5262158

; GENERAL INFORMATION:
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TYPE: AMINO ACID
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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USA
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ANTI-SENSE: NO
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2452.5
2441.5
2237.5
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GENERAL INFORMATION:
APPLICANT: Poncerrada, Luis R
APPLICANT: Payne, Jewel M
APPLICANT: Payne, Jewel M
APPLICANT: Sick, August J
TITLE OF INVENTION: No. 5366892el Coleopteran-Active Bacillus
TITLE OF INVENTION: Coleopteran-Active and a No. 5366892el Gene Encoding
TITLE OF INVENTION: Coleopteran-Active Toxin
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
1019 RLQQAMNLYDLRNAIPNGDFRNGLSDWATSDVNVQQLSDTSVLVIPNMNSQVSQQFTVQ 1078
1009 RLQQAMNLYDQRNAIPNGDFRNGLSNWNATPGVEVQQINHTSVLVIPNWDEQVSQQFTVQ 1068
                                                                             1069 PNORYVLRVTARKEGVGNGYVSIRDGGNQSETLIFFSASDYDTNGVYNDOTGYTKTVIFI 1128
                                                            PNYRYVLRVTARKEGVGDGYVI I RDGANQTETLI FNI CDDDTGVLSADQTSY I TKTVRPT
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Best Local Similarity 66.1%; Pred. No. 2.3e-285;
Matches 773; Conservative 144; Mismatches 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTIER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PLEATING SYSTEM: PC-DOS/MS-DOS 5.0
SOFTWARE: PALENTIN RELEASE #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,180A
FILING DATE: 19920102
CLASSIFICATION: 435
ATTOMNEY/AGENT INPORMATION:
NAME: Saliwanchik, Roman
TELECOMMUNICATION: NUMPRRATION:
TELECOMMUNICATION: 1904-375-8100
TELEFRAN: 904-375-8100
                                                                                                                                         PSTEQUWIDMSETEGUPNIESVELVLEEE 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                A-1
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STREET: 2421 N.W. 418t Street, Ste
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
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US-07-1812-180A-2
; Sequence 2, Application US/07812180A
; Patent No. 5366892...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLEGULE TYPE: protein
HYPOTHETICAL: YES
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LIBRARY: FONCERRADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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US-07-812-180A-2
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                                                                                                                                           RIPISSSTVOTGIGIVGQVLGALGVPFAGQIASPYSPIVGQLMPSSTVSVWEMIMKQVED 120
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                                                                              1 MSPNNONEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
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                                                  Gaps
                                               14;
                  Length 1157;
                  Query Match 66.3%; Score 4007; DB 1; Length 1 Best Local Similarity 66.1%; Pred. No. 2.3e-285; Matches 773; Conservative 144; Mismatches 238; Indels
                                                                                                                                             61
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61 ETPISSSTVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVED 120
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                                                                                                                                                                                   APPLICANT: Michaels, Tracy Ellis
APPLICANT: Poncerrada, Luis
APPLICANT: Poncerrada, Luis
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 418t Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/08/014,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
PILLING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
PILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: 07/808,316
PILING DATE: 16-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/POCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Bacillus thuringiensis kumamotoensis
                                                                                                                         ; Sequence 2, Application US/08315468
; Patent No. 5554534
; GENERAL INFORMATION:
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IMMEDIATE SOURCE:
LIBRARY: Lambdagem (TM) - 11
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    32606
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                                                                                                      US-08-315-468-2
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  240
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                                                                                   420 LANYYQKAYGVPGSWFHMVKR--GTSSTTAYLYSKTHTALQGCTQVYBSSDEIPLDRTVP
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                                                                                                               GENERAL INFORMATION:
APPLICANT: Uyeda, Kendrick A.
APPLICANT: Bradfisch, Gregory A.
APPLICANT: Bradfisch, Gregory A.
TITLE OF INVENTION: Process for Controlling Lepidopteran Pests
NUMBER OF SEGUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
66.3%; Score 4007; DB 3; Length 1.
Best Local Similarity 66.1%; Pred. No. 2.3e-285;
Matches 773; Conservative 144; Mismatches 238; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | IMMEDIATE SOURCE:
| CLONE: B. coll NM522 (pMYC1638), NRRL B-18751
| US-07-941-650A-2
1129 PYTDQMWIBISETEGTFYIESVELIVDVE 1157
                                                                                                                                                                                                                 ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,650A
FILING DATE: 1920908
CLASSIFICATION A435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/758,020
FILING DATE: 12-8EP-1991
PRIOR APPLICATION NUMBER: US 07/658,335
FILING DATE: 21-FEB-1991
PRIOR APPLICATION NUMBER: US 07/658,335
FILING DATE: 16-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
TELECOMMUNICATION NUMBER: 31,794
TELECOMMUNICATION NUMBER: 31,794
TELEPHONE: 204-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                Sequence 2, Application US/07941650A Patent No. 6294184
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MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
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181 SIPSPAVSGHEVLLLAVYAQAVNLHLLLLLEDASIPGEEWGFTPGEISRPYNRQVQLTAE 240
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XSDXCVKMYNTGLDKLKKGTNAASMLKYHQFRREMTLLVLDLVALPPNYDTRTYPIETTAQ 300
                                                                                                                                                                                                     241 YSDYCVKWYKIGLDKIKGTISKSWINYHQPRREWTLIVIDLVALFPNYDTHMYPIETTAQ 300
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                                                                                                                                                                                                                                                                        LPLNNTEYLEYWYGHSIKYKNT-NASSALERNYGTITSNKIKYYDLANKDIFQVRSLGAD 419
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                                                  LIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFV 180
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                                                                                                                                    YSDYCVKWYKIGLDKIKGTISKSWI.NYHQPRREMTILVI.DIVALPPNYDTHMYPIETTAQ
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299 61 ETPISS-STVQTGIGIVGQVLGALGVPPAGQIASPYSPIVGQLWPSSTVSVWEMIMKQVB 119 OLTREVYTOPIVFNRETSGGFCRRWSLN----SDI-----SPSEVESAVIRSPHLPDIL 349 :||||::|||: ELTREIPTDFV-----GSYVTGQSSTLISWYDMIPAALPSPSTLEN-LLRKPDPPTLL 352 9 9 1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNANYKDYLRMSEGENPELFGNP DLIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTA Ouery Match 60.6%; Score 3662.5; DB 1; Length 1149; Best Local Similarity 63.8%; Pred. No. 4.6e-260; Matches 752; Conservative 109; Mismatches 257; Indels 61; and COMPUTER KEADMADLE FURN:

MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: 19920723
FILING DATE: 19920723
FLING DATE: 19920723
CLASSIFICATION NUMBER: US/07/915,203
FLING DATE: 19920723
ATTORNEY/AGENT INPORMATION:
NAME: Saliwanchik, David R.
REPERBENCE/POCKET NUMBER: M/K 301
TELEPHONE: 904-372-800
TELEPHONE: 904-372-5800
INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS: APPLICANT: Voba, Michio
APPLICANT: Voba, Michio
APPLICANT: Ivahana, Hidenori
APPLICANT: Sato, Reiichi
APPLICANT: Sato, Reiichi
APPLICANT: Gqiwara, Katautoshi
APPLICANT: Gqiwara, Katautoshi
APPLICANT: Sakanaka, Kazunobu
APPLICANT: Asano, Shouji
AP : 1149 amino acida AMINO ACID TOPOLOGY: linear MOLECULE TYPE: protein COMPUTER READABLE FORM: SD ZIP: 32606 COUNTRY: US-07-915-203-2 300 301 ò

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NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Matches 752; (
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               SEI BFYTTRAGLPLNNT-EYLEYWVGHSI KYKNTNASSALBRNYGTITSNKI KYYDLANK
                                                             DI POVRSLGADLANYYAQVYGVPYASFITLDKNIGSGSVGGFIYSKPHITMQVCTQNYNI
                                                                                  DIYRV--VWTYIGRYTNSLLGVNPVTF-YPSNNTQK-----TYSKP----KQFAGGIKT
                                                                                                             469 ID---EIPPENBPLSRGYSHRLSHITSYSFSKNASSPARYGNLPVPAWTHRSADVTNTVY
                                                                                                                        526 SDKITQIPVVKAHTLVSGTTVIKGPG-PTGGNILKRTSSGPLAY---TSVSVKSPLSQRY
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Iwahana, Hidenori
Sato, Relichi
Suzuki, No. 5747450ukazu
Ogiwara, Katsutoshi
Sakanaka, Kazunobu
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Patent No. 5747450
GENERAL INFORMATION:
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APPLICANT: Iwahana,
APPLICANT: Suzuki, N
APPLICANT: Ogiwara,
APPLICANT: Ogiwara,
APPLICANT: Sakanaka,
APPLICANT: Hori, Hid
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                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/272,887
FILING DATE: 08-UUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION NATA:
APPLICATION NUMBER: US 07/915,203
FILING DATE: 23-UUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60.6%; Score 362.5; DB 1; ilarity 63.8%; Pred. No. 4.6e-260; Conservative 109; Mismatches 257;
ADDRESSE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CTTY: Gainesville
STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELEPHONE: 904-375-8100
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
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                                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1149 amino acids
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TOPOLOGY: linear
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Kawasugi, Tadaaki ENTION: No. 5747450el Microorganism and Insecticide

Hori, Hidetaki Asano, Shouji

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DIFQVRSLGADLANYYAQVYGVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNT 468
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                                  PatentIn Release #1.0, Version #1.25
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60.6%; Score 3662.5; DB 2
Best Local Similarity 63.8%; Pred. No. 4.6e-260;
Matches 752; Conservative 109; Mismatches 257;
                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION IDATA:
APPLICATION NUMBER: US 08/272,887
PILING DATE: 08-ULL-1994
APPLICATION NUMBER: US 07/915,203
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,449
                                                                                                                                                                                                                                                                                           NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKEF NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-800
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 1149 amino acids
amino acid
                                                                                                                                                                                                                                              FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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US-08-789-449-2
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                                                                                                                                                      RARIRYASTINLRLFVTIS-----GTRIYSINVNKIMNKGDDLTFNTFDLATIGTA-F 633
            IDSGERLTYEN---YQSYSHRVSYITSPRIKSTGGTV--LGVVPIFGWTHSSASRNNFIY 509
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                                                             SDKITQIPVVKAHTLVSGTTVIKGPG-FTGGNILKRTSSGPLAY---TSVSVKSPLSQRY
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TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NICDDDTGVLSTDQTSYITKTVBFTPSTEQVWIDMSETE 1145
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2421 N.W. 418t Street, Suite A-1
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Ohba, Hidenori
Sato, Relichi
Suzuki, No. 5824878ukazu
Ogiwara, Katsutoshi
Sakanaka, Kazunobu
Hori, Hidetaki
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1169;
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 52.2%; Score 3152; DB 1; Length 1. Best Local Similarity 54.0%; Pred. No. 1.4e-222; Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                            L. Foncerrada
            NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA73.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
                                                                                                                                                                                                                                                                                                                                                          LambdaGKM-11 library of
                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus thuringiensis STRAIN: kumamotoensis
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
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                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                       amino acid
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CLONE: 50C(b)
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ANTI-SENSE: NO
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               GIMSSDSHAFSFHIDTGEIDLINENTGIWIVFKIPTTNGNATLGNLEFVEEGFLSGETLEW
                                                                                                                                                                                                                                                                                                                                                            QTSVTDYQVNQAANLIECLSDELYPNEKRMLWDAVKEAKKLVQARNLLQDTGFNRINGEN
                                                                                                                                                                                                                                          CHMSSDSHAPSPHIDTGBIDLNENTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLER
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                                                                                   QTSVTDYQVNQAANLVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRINGEN
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                                                                                                                                                                        GWTGSTGIEVVEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDBSLLKPYTRYKLKGFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INC. 23-29-29-4

GENERAL INCORPORATION:

APPLICANT: Michaels, Tracy Ellis

APPLICANT: Poncerrada, Luis

APPLICANT: Narva, Kennel

TITLE OF INVENTION: Process for Controlling Scarab Pests

TITLE OF INVENTION: with Bacillus thuringiensis Isolates

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1114 NICDDDTGVLSADQTSYITKTVRFTPSTEQVWIDMSETE 1152
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ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPEM PLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/014,941
PILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
PILING DATE: 30-JAN-1992
PRICA APPLICATION DATE:
APPLICATION NUMBER: 07/808,316
PILING DATE: 16-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08315468
Patent No. 5554534
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
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REGISTRATION NUMBER:
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           GWTGSTGIEVAEGDVLPKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPI
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APPLICANT: JANSENS, STERAN
APPLICANT: VAN AUDENHOUE, KATRIEN
APPLICANT: PEFEREN, MARNIX
APPLICANT: VAN ARASSEN, ROEL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THEIL
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: BLTCh, SEWART, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STRIE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUTRIENT APPLICATION DATA:
APPLICATION NUMBER: US/08/532,547
FILLING DATE: 06-DEC-1996
FILLING DATE: 06-DEC-1996
ALTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/08532547; Patent No. 2861543; GENERAL INFORMATION: APPLICANT: LAMBERT, BART
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ESVELIVDVE 1169
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                                                                                                                                                                                                                                     Length 1157;
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REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
                                                                      TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: amino acid
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HOLECULE TYPE: protein
US-08-532-547-5
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52.3%;
          TOPOLOGY: linear
MOLECULE TYPE: protein
amino acid
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 ; TYPE: amin
; TOPOLOGY:
; MOLECULE TYPE
US-08-379-6568-5
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                                                                                                                                                                                                                                                                   SHWDAQVSQQLRVNPNCKYVLRVTARKVGGGGTYVTIRDGAHHQBTLTFNACDYDVNGTY 1114
                                                                                                                                MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004
                                                                                                                                               FHIDTGEIDLMENTGIWVVFKIPTTNGYATLGNLELVEBGPLSGETLERAQQQEQQWQDK 944
                                                                                                  875 SYINTGDLNASVDQQIWVVLKVRTTDGYATLGNLELVEVGPLSGESLERRQRDNAKWNAE 934
                          RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lambert Bart
APPLICANT: Lambert Bart
APPLICANT: Jansens, Stefan
APPLICANT: Van Audenhove, Katrien
APPLICANT: Veferoen, Marnis.
APPLICANT: Peferoen, Marnis.
APPLICANT: Peferoen, Marnis.
AUTILB OF INVENTION: THEIR INSECTICIDAL PROTEINS
NUMBER OP SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                                                        1125 ADQTSYITKTVEFTPSTEQVWIDMSETECVPNIESVELVLEBE 1167
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1115 VNDNSYITEEVVFYPETKHMWVEVSESBGSFYIDSIEFIETQE 1157
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COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
WEDIUM TYPE: TBM PC Compatible
COMPUTER: TBM PC Compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-104P
TELECOMMUTICATION INFORMATION:
TELEFHONE: (703) 205-8050
TELEFAX: (703) 205-8050
TELEFAX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFLICATION WOMEN: US/US/3/9,0369
PRICE APPLICATION DATA:
APPLICATION NUBER: PCT/EP93/01820
PILING DATE: 12-JULY-1993
PRICE APPLICATION DATA:
APPLICATION NUBER: EP 93400949.9
PRICE APPLICATION DATA:
PRILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/379,656B
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Patent No. 5885571
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STATE: Virginia
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                   VAKIPSPAISGQEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417 GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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                                                                       1 MSPNNQNBYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELPGNP
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                                     42;
Length 1157;
                                     Indele
                                     Matches 619; Conservative 195; Mismatches 327;
Score 3123; DB 2;
Pred. No. 1.9e-220;
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QY 1 MSPANQNEYBILDASSTSVSDNSVRYPLANDQTTTLQAMAYKDYLRMSEGENPBL.PGNP 60 :	Qy 61 ETFISS-STVOTGIGIVGOVLGALGVPRAGQIASFYSFIVGOLWPSSTVSVWEMINKQVB 119	QY 120 DLIDQKITDSVRKTALAGLGGLGDGLDVYQKSLKNMLKNRNDTRARSVVVTQXIALBLDF 179 : :: : - - - - - - - - - - -	QY 180 VAKIPSFAISGQEVPLLSSYAQAANLHILIRDASIFGAEWGFTPGRISTFYDRQVTRTA 239 181 VAAIPLFAVNGQQVPLLSSYAQAVNLHLLLLXDASLFGEGWGFTQGRISTYYDRQLBLTA 240	QY 240 QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLIVLDLVALPPNVDTRTYPIETTA 299 : ::	QY 300 QLTREVYTDPIVERRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDILSEIBFYTTRA 359 Db 301 QLTREVYTDPIVENPPANVGLCRRWGTNPYNTFSELENAPIRPPHLFDRLNSLTISSNR- 359	OY 360 GLPLNNIEYLEYWVGHSIKYKNINASSALERNYGTITSNKIKYYDLANKDIFQVRSL 416	Qy 417 GADLANYYAQVYGVPYASFTLLDRNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP 474 :	Qy 475 ENEPLSRGYS-HRISHITSYSPSKN-ASSPARYGALPVFAWTHRSADVTNTVYSDKITOI 532 1	QY 533 PVVKAHTLVSGTTVJKGBQFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASITN 592	Qy 593 IRLFVTISGTRIYSINVNKTWANGDDLTFNTFDLATIGTAFTFSNYSDSLTVGA 646 579 FSIRVLRGGVSIGDVRLGSTWANGQBLTYRSFFTREFTTGPRNPFTFTQAQBILTVNA 638	QY 647 DSPASGEVYVDKPELIPVNATPEAREDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAA 706 ::: : :	OY 707 NLVECLSDELYPREKRIMDAVKBAKRLVQARNILQDTGFNRINGENGWTGSTGIEVA 764	Oy 765 BGDVLPKDRSLRLTSARRIDTETYPTYLXQQIDBSLLKPYTRYKLKGFIGSSQDLRIKLI 824	QY 825 RHRANQIVKNVPDNLLPDVLFVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAFS 884	OY 885 FHIDTGEIDLARRYGIWVVFKIPTTAGYATLGALELVEEGPLSGETLERAQOEQQWQDK 944	OY 945 MARKRGASEKAYYAAKQAIDRLPADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPB 1004 :	CY 1005 IPGMNYTSFTELTNRLQQAMNLYDLENAIPNGDFRNGLSDWNATSDWNVQQLSDTSVLVI 1064
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3 1004	1064	1124															**
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YODOKINSGVEMSDMIAAQMIVOSIPYVYNDALPE 		GVLS NGTY	ETEGVFNIESVELVLEER 1167 - - - - ESEGSFYIDSIEPIETQR 1157			THURINGIENSIS STRAINS AND	CLDAL PROTEINS SCH & BIRCH	ite 500 Bast		, Version #1.25 38	820	6,	œ.	d90			Length 1157; Indels 42; Gaps
yaakoaidrlfadyodokinsgvemsdmiaaonivosipyvyndalde 		GVLS NGTY	PIPSTRQVWIDMSETEGVFNIESVELVLEEB 1167 : : :: : : : TYPETTGHMWUEVSESEGSFYIDSIBPIETQB 1157		US/08455838 	Stetan blove, Katrien Marnix NEW BACILLUS THURINGIENSIS STRAINS AND	THEIR INSECTICIDAL PROTEINS 5 SS: STEWART, KOLASCH & BIRCH	ouse Road, Suite	W.i y disk ompatible	PC-DOS/MS-DOS Release #1.0, Version #1.25 NTA: US/08/455,838	X-1995 .A: - PCT/EP93/01820 ILY-1993	EP 93400949. 1993	EP 92402358.8 KG-1992 KATION: COMBATO R.	i: 30,330 MRBER: 2121-106P ORMATION: 05-8000	-8050 NO: 5: TCS:	cids	 \$\$\frac{1}{8}\$; Score 3123; DB 3; Length 1157; \$\$\frac{1}{8}\$; Pred. No. 1.9e-220; \$\$\frac{1}{9}\$; Mismatches 327; Indels 42; Gaps
945 MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 	1005 IPGMNYTSFTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI :		1125 ADQTSYITKTVEFTPSTBQVWIDMSETBGVFNIESVELVLEER 1167 :	ហុ	5 33	APPLICANT: Jansens, Steran APPLICANT: Van Audenbove, Katrien APPLICANT: Pefercen, Marnix IITLE OP INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND	64	10 Gatehouse Road, Suite s Church ginia .S.A.	ZIF: 22042 COMPUTER READBLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER: IBM PC compatible	STEM: PO RECTION DAY TUMBER:	FILING DATE: 31-MAY-1995 PRIOR APPLICATION DATE: PAPLICATION NUMBER: PCT/RP93/01820 FILING DATE: 12-JULY-1993	A: EP 93400949. R-1993 A:	EP 92402358 -1992 TION:	KBER: 30,3 F NUMBER: INFORMATIC 3) 205-8000	TELEFAX: (703) 205-8050 TELEX: 248345 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:	LENGTH: 1157 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein	ore 3123; DB 3; Length 1157; red. No. 1.9e-220; Mismatches 327; Indels 42; Gaps

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995 IPGINYBIYTELSDRLQQASYLYTSRNAVQNGDFNSGLDSWNTTMDASVQQDGNMHFLVL 1054
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                            QYSDYCVKWYNTGLDKLKGTNAASMLKYHQPRREWTLLVLDLVALPPNYDTRTYPIETTA
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; Sequence 5, Application US/09471177
; Patent No. 6448226
; GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
; APPLICANT: JANSENS, STEFAN
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APPLICANT: JANBERY, STEFAN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN ARESEN, ROEL
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
TITLE OF INVENTION: SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STREET: VIGINIA
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                                                                                  1125 ADQTSYITKTVEFTPSTEQVWIDMSETEGVFNIRSVELVLERE 1167
                                                                                                               SUNDICENTIFIED STREET S
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ZIP: 22040-0147

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,809
PILING DATE: US-PEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: SVENSSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-135P
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                   Sequence 5, Application US/09019809;
Patent No. 6143550;
GENERAL INFORMATION:
APPLICANT: LAMBERT, BART
APPLICANT: JANSENS, STEFAN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN ALB, JEROEN
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN AARSSEN, ROEL
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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US-09-019-809-5
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1005 IPGMNYTSFTELTRRLQQAMNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                       NIVECLSDELYPNEKRMLWDAVKRAKRLVQARNILQDTGFNRING--BNGWTGSTGIEVA
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                     GADLANYYAQVYGVPYASPTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
                                                                                             475 ENEPLSRGYS-HRLSHITSYSFSKN-ASSPARYGNLPVFAWTHRSADVTNTVYSDKITQI
                                                                                                                   533 PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
                                                                                                                                                                                                                                                  593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTP---DLATIG---TAPTFSNYSDSLTVGA
                                                                                                                                                                                                                                                                                                                              647 DSFASGGEVYVDKFELIPVNATFEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAA
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; Sequence 72, Application US/09002285
; Patent No. 6369213
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wicker, Carol
APPLICANT: Walex, Kenneth B.
APPLICANT: Walex, Michelle
APPLICANT: Walex, Carol
APPLICANT: Walex, Michelle
APPLICANT: Walex, Dicket, Brian
APPLICANT: Walex-Oxhoff, Lioyd & Saliwanchik
STREEF: 2421 N W. 418t Street, Suite A-1
STREEF: Saliwanchik, Lloyd & Saliwanchik
STREEF: Saliwanchik, Lloyd & Saliwanchik
STREEF: Saliwanchik Alberts
STREEF: Saliwanchik Street, Suite A-1
STREEF: Saliwanchik Street, Suite A-1
STREEF: Saliwanchik
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APPLICANT: VAN AUDENHOVE, KATRLEN
APPLICANT: PERERGEN, MARNIX
APPLICANT: PREFROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN RARSSEN, ROBL
TITLE OF INVENTION: INSECTICIDE FROTEINS.
TITLE OF INVENTION: INSECTICIDE PROTEINS.
TITLE OF INVENTION: STEWART, KOLASCH & BIRCH, LLP
TITLE OF INVENTION: STEWART, KOLASCH & BIRCH, LLP
CORRESPONDENCE ADDRESS:
ADDRESSER: BLYCH, SteWART, KOLASCH & BIRCH, LLP
STREET: P.O. BOX 747
CITY: Falls Church
STREET: P.O. BOX 747
COUNTRY: USA
ZIP: 22040-0747
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DESCRIPTION OF STETMEN PC DOSS/MS.
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Matches 619; Conservative 195; Mismatches 327; Indels
                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/471,177
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NDBER: US/09/019,809
FILING DATE: 02-FEB-1998
ATTORNET/AGENT INFORMATION:
NAME: SYENSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-135P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-589-477-72
; Sequence 72, Application US/09589477
; Patent No. 6570005
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1156;
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                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US 08/886,615
FILING DATE: 1-UUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERNEK/POCKET NUMBER: MA-701C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 372-5800
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acid8
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: PATENTIN
SOOTWARE: PATENTIN
APPLICATION NUMBER: US/09/002,285
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; MOLECULE TYPE: protein
US-09-002-285-72
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                                                                                                                   FILING DATE:
CLASSIFICATION:
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1006 PERNYTSFTELTNRIQOANLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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                                                                                                                                                                                                                                                                                                                             826 HRANGIVKNVPDNILLPDVLPVNSCGGIDRCSEQQYVDANLALENDAGENGNMSSDSHAPSF 885
                                                                                                                                                                                                                                                                                                                                                                                                              886 HIDTGEIDLNENTGIWVVFKIPTTNGYATLGNLELVERGPLSGETLERAQQQEQQWQDKM 945
                                                                                                                                                                                    LVECLSDELYPNEKRMEMDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVAE
                                                                                                                                                                                                                                              766 GDVLFKDRSLRLTSARBIDTETYPTYLYQQIDBSLLKPYTRYKLKGPIGSSQDLBIKLIR
                                                                                                                                                                                                                                                                                                                                                  593 LALFVIISGIRIYSINVNKTWAKGDDLIFNTFDLATIGT-----AFTFSNYSDSLTVGAD
                                                                             648 SPASGGEVYVDKPELIPVNATFEAEEDLDVAKKAVNGLFTSKKDALQTSVTDYQVNQAAN
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APPLICANT: Wicker, Carol
APPLICANT: Narva, Remeth B.
APPLICANT: Walz, Michelle
APPLICANT: Stockhoff, Brian
TITLE OF INVENTION: Toxins Active Against Pests
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSER: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville STATE: Plorida
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639 GVSTGSEYFIDRIBIIPVNPAREABEDLEAAKKAVANLFTRTRDGLQVNVTDYQVDQAAN

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61 ETFISS-STVQTGIGIVGQVLGALGVPFAGQIASPYSFIVGQLWPSSTVSVWEMIMKQVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLIDOKITDSVRKTALAGLØGLGDGLDVYØKSLKNWLENRNDTRARSVVVTØYIALBLDF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTPYDRQVTRTA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OLTREVYTOPIVFNRETSGGPCRRWSLNSDISPSRVESAVIRSPHLPDILSBIBFYTTRA 359
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                                                                                                                                                                                                                                                                                                                                                                                        41; Gaps
                                                                                                                                                                                                                                                                                                                                                         Length 1156;
                                                                                                                                                                                                                                                                                                                                                         Query Match 51.3%; Score 3100.5; DB 4; Length Best Local Similarity 52.0%; Pred. No. 8.5e-219; Matches 615; Conservative 196; Mismatches 330; Indels
PELICATION NUMBER: US 08/886,615
FILING DATE: 1-JUL-1997
CLASSIFICATION: 1-JUL-1997
FRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION: 1-JUL-1996
CLASSIFICATION: 39,355
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8000
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 1156 amino acids
                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                       PGYMYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVIP 1065
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708 LVECLSDELYPNEKRMENDAVKRAKRLVQARNILLQDTGFNRING - ENGWTGSTGIEVAE
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Search completed: June 21, 2004, 13:40:18 Job time: 27 8ecs

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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 08-UL-1994
APPLICATION NUMBER: US 07
                                                                                                                           FILING DATE: 23-JUL-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                       1149 amino acids
                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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Matches 752;
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US-08-789-449-2
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                                                                                                                                                                             QTSVTDYQVNQAANLVECLSDELYPNEKRHIMDAVKEAKRLVQARNILQDTGFNRINGEN 753
                                                                            RARIRYASTTNLRLFVTIS-----GTRIYSINVNKTMNKGDDLTFNTFDLATIGTA-F 633
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IDSGEELTYEN---YQSYSHRVSYITSPEIKSTGGTV--LGVVPIFGWTHSSASRNNFIY 509
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                                                                                                                             TPSNYSDSLTVGADSPASGGEVYVDKFBLIPVNATFBAEBDLDVAKKAVNGLFTSKKDAL
                                                                                                                                                   GISGSSRIPDISITKEAGAANLYIDRIEFIPVNTLFEAEEDLDVAKKAVNGLFTNEKDAL
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                          SDKITQIPVVKAHTLVSGTTVIKGPG-FTGGNILKRTSSGPLAY---TSVSVKSPLSQRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kawasugi, Tadaaki
TITLE OF INVENTION: No. 5824878el Microorganism and Insecticide
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NICDDDTGVLSTDOTSYITKTVEFTESTEOVWIDMSETE 1145
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STREET: 2421 N.W. 41st Street, Suite A-1
STATE: Galnesville
STATE: FL
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohba, Michio
Iwahana, Hidenori
Sato, Relichi
Suzuki, No. 5824878ukazu
Ogiwara, Katsutoshi
Sakanaka, Kazunobu
Hori, Hidetaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08789449
Patent No. 5824878
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT:
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301 ELTREIFTDPV-----GSYVIGQSSTLISWYDMIPAALPSFSTLEN-LLRKPDFFTLL 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VAKIPSPAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYSDYCVKWYNTGLDKLKGTNAASWLKYHOFRREMTLLVLDLVALPPNYDTRTYPIETTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 QEIRMYTS---FRQNGTIEYYNYWGGQRLTLSYIYGSSP--NKYSGVLAGAEDIIPVGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1149;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 63.8%; Pred. No. 4.6e-260;
Conservative 109; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.6%; Score 3662.5;
63.8%; Pred. No. 4.6e-
                                                                                                                            US 08/272,887
                                                                                                                                                                      US 07/915,203
                                                                                                                                                                                                                                 NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/K 301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEPAX: 904-372-5800
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 OLTREVYTOPIVPNRETSGSPCRRWSLNSDISPSEVESAVIRSPHLFDILSEIBFYTTRA 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180 VAKIPSFAISGOEVPLLSVYAQAANLHLILLRDASIPGAEWGFTPGEISTFYDRQVTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 52.2%; Score 3152; DB 1; Length 1: Best Local Similarity 54.0%; Pred. No. 1.4e-222; Matches 653; Conservative 179; Mismatches 294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: LambdaGEM-11 library of L. Foncerrada
CLONE: 50C(b)
                                                  REGISTRATION NUMBER: 31,794
REFERENCE/DOCKGI NUMBER: MA73.C2
TELECOMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-375-800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 amino acids
TYPER: SAME ACTION ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Bacillus thuringiensis
STRAIN: kumamotoensis
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE: 50C IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: Y
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNMSSDSHAFSPHIDTGEIDLNBNTGIWVVPKIPTTNGYATLGNLELVEBGPLSGBTLER
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                                  634 TPSNYSDSLTVGADSPASGGEVYVDKPELIPVNATPEAEBDLDVAKKAVNGLFTSKKDAL
                                                                                                                                                                                                                                                                             754 GWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Michaels, Tracy Ellis
APPLICANT: Moncerrada, Luis
APPLICANT: Narva, Kenneth APPLICANT: Narva, Kenneth Process for Controlling Scarab Pests
TITLE OF INVENTION: with Bacillus thuringiensis Isolates
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107 NICDDDTGVLSTDQTSYITKTVEFTESTEQUWIDMSETE 1145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/315,468
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STREET: 2421 N.W. 418t Street, Suite A-ICITY: Gainesville
STATE: FL
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/014,941
PILING DATE: 01 FEB 1993
APPLICATION NUMBER: 07/828,430
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA: 07/808,316
PRIOR APPLICATION NUMBER: 07/808,316
FILING DATE: 16-DEC-1991
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Patent No. 5554534
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360 -FPV-SSNFMDYWSGHTLRRSYLNDSAVQEDSYGLITTRATINPGVDGTNR----IEST 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 QLTREVYIDPIVFNPPANVGLCRRWGTNPYNTFSELENAFIRPPHLFDRLNSLTISSNR- 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 VAKIPSFAISGOEVPLLSVYAQAANLHLLLLRDASIFGAEWGFTPGEISTFYDRQVTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 GADLANYYAQVYGVPYASFTL - LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP
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1 MARANQNEYEIIDAPHCGCPSDDDVRYPLASDPNAALQNAVYKDYLQMTDEDYTDSYINP
                                                                                                                                                                                                                                                                                             1 MSPNNONBYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                               Length 1157;
                                                                                                                                                                                                                            Query Match
51.7%; Score 3123; DB 2; Length 11:
Best Local Similarity 52.3%; Pred. No. 1.9e-220;
Matches 619; Conservative 195; Mismatches 327; Indele
          REPERENCE/DOCKET NUMBER: 2121-109P
TELECOMPUTICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
TELEPAX: 248345
INFORMATION FS SEQ ID NO: 5: SRQUENCE CHARACTERISTICS: LENGTH: 1157 amino acids
TYPE: amino acid
TOPOLOGY: linear
30,330
                                                                                                                                                                          , MOLECULE TYPE: protein US-08-532-547-5
REGISTRATION NUMBER:
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                                                                                                                               GWTGSTGIEVAEGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFI 813
                                                                                                                                              GSSQDLEIKLIRHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGEN 873
                                                                                                                                                                                                                                                                GNMSSDSHAPSFHIDTGEIDLNEWTGIWVVFKIPTTNGYATLGNLELVEEGPLSGETLER 933
                                                                                                                                                                                                                                                                                   SVNASSNIQRESIGIQINTNIPILDRIBPIPVDETYBABTDLBAAKKAVNALFTNTKDGL
TVGADS------PASGGEVYV-DKFBLIPVNATFEAEEDLDVAKKAVNGLPTSKKDAL
                                                               QTSVTDYQVNQAANLVECLSDBLYPNBKRMLWDAVKEAKRLVQARNLLQDTGFNRINGEN
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APPLICANT: VAN AUDENGOVE, KATRIEN
APPLICANT: VAN ALDENGOVE, KATRIEN
APPLICANT: VAN ARSSEN, ROEL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND TITLE OF INVENTION: INSECTICIDAL PROTEINS.

NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
STREET: P.O. BOX 747
STREET: P.O. BOX 747
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CITY: Falls Church
STATE: Virginia
COUNTRY: USA
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APPLICATION NUMBER: US/08/532,547
FILING DATE: 06-DEC-1996
CILSSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LAMBERT, BART
APPLICANT: JANSENS, STEFAN
APPLICANT: VAN AUDENGOUS, KATRIEN
APPLICANT: PEFEROEN, MARNIX
APPLICANT: VAN RIE, JEROEN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-532-547-5
; Sequence 5, Application US/08532547
; Patent No. 5861543
; GENERAL INFORMATION:
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                                                             PHIDTGEIDLINENTGIWVVPKIPTINGYATLGNLELVEEGPLSGETLERAQQQEQQWQDK 944
                                                                                                                                       HHHKVHLVKAVPDNLVSDTYSDGSCSGINRCDEQHQVDMQLDAEHHPMDCCEAAQTHEFS
                                                                           SYINTGDLAASVDQGIWVVLKVRTTDGYATLGALELVEVGPLSGESLEREQRDAAKWABE
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RHRANQIVKNVPDNLLPDVLPVNSCGGIDRCSEQQYVDANLALENNGENGNMSSDSHAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Lambert Bart
APPLICANT: Jansens, Stefan
APPLICANT: Van Audenhove, Katrien
APPLICANT: Peferoen, Marnix
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
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ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,656B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSER: BIRCH, STEWART, KOLASCH & BIRCH STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/379,656B
PILING DATE: 23-MAR-1995
RIOR APPLICATION DATE:
APPLICATION DATE: T-1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/RP93/01820
FILING DATE: 12-JULY-1993
RIOR APPLICATION DATE: APPLICATION NUMBER: BP 93400949.9
FILING DATE: 09-APR-1993
PRIOR APPLICATION NUMBER: BP 92402358.8
FILING DATE: 27-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAMME: SVENSSON, LEGGRAGER.
NAMME: SVENSSON, LEGGRAGER.
REGISTRATION NUMBER: BP 92402358.8
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Patent No. 5885571
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STI
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                                                                                                                                                                                                   61 BTFISS-STVQTGIGIVQQVLGALGVPPAGQIASPYSRIVGQLWPSSTVSVWEMIMKQVB
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                                                                                                                                      42;
                                                                                                Length 1157;
                                                                                                                                      Indels
                                                                                              tch 51.7%; Score 3123; DB 2;
al Similarity 52.3%; Pred. No. 1.9e-220;
619; Conservative 195; Mismatches 327;
                TOPOLOGY: linear
MOLECULE TYPE: protein
amino acid
                                                                                                                 Best Local Similarity
Matches 619; Conserv
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MARKRGASEKAYYAAKQAIDRLFADYQDQKLNSGVEMSDMLAAQNLVQSIPYVYNDALPE 1004
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                                                          NIVECLSDELYPNEKRMLWDAVKEAKRLVQARNLLQDTGFNRING--ENGWTGSTGIEVA 764
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                                                                                                                                                                                                                                                                  360 GLPLNNTEYLEYWVGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIPQVRSL 416
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              DLIDOKITDSVRKTALAGLOGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                          417 GADLANYYAQVYGVPYASFTL--LDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDBIPP
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MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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SHWDAQVSQQLRVNPNCKYVLRVTRAKVGGGGGYVTIRDGAHHQETLTFNACDYDVNGTY 1114
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                                                             I PGWNYTSPTELTNRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI
                                                                                                                          PNWNSQVSQQPTVQPNYRYVLRVTARKEGVGDGYVI IRDGANQTETLTFNI CDDDTGVLS
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APPLICANT: Jameens, Stefan
APPLICANT: Van Audenbove, Katrien
APPLICANT: Peferoen, Marnix
TITLE OF INVENTION: THEIR INSECTICIDAL PROTEINS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 Bast
CITY: Palls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
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                                                                                                                                                                                       ADQTSYITKTVEPTPSTEQVWIDMSETEGVFNIESVELVLEEE 1167
                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,838
FILING DATE: 31-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/01820
FILING DATE: 12-JULY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 93400949.9
FILING DATE: 09-APR-1993
PRIOR APPLICATION NUMBER: B 92402358.8
FILING DATE: 27-AUG-1992
APPLICATION NUMBER: B 92402358.8
FILING DATE: 30-AUG-1992
APPLICATION NUMBER: B 92402358.8
FILING DATE: 30-AUG-1992
APPLICATION NUMBER: 30,330
REGISTRATION NUMBER: 30,330
REGERENCE/DOCKET UNDBER: 2121-106P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                               US-08-455-838-5; Sequence 5, Application US/08455838; Patent No. 6028246; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
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995 IPGINYELYTELSDELQQASYLYTSENAVQNGDFNSGLDSWYTTMDASVQODGNMFFLVL 1054
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                  240 QYSDYCVKWYNTGLDKLKGTNAASWLKYHQPRREMTLLVLDLVALPPNYDTRTYPIETTA 299
241 KYTNYCETWYNTGLDRLKGTNTESWLRYHQPRREMTLVVLDVVALPPYYDVRLYPTGSNP 300
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US-09-471-177-5
US-09-471-177-5
Sequence 5, Application US/09471177
Patent No. 6448226
GENERAL INFORMATION:
APPLICANT: LAMBERT BART
APPLICANT: JANSENS, STEFAN
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APPLICANT: LAMBERT, STEPAN
APPLICANT: JANSENS, STEPAN
APPLICANT: VAN AUDENHOVE, KATRIEN
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN ARSSEN, ROEL
TITLE OF INVENTION: NEW BACTLLUS THURINGIENSIS STRAINS AND THBIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES:
ADDRESSES: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STREET: Virginia
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                                                     1167
                                                                                        1157
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWBER: US/09/019,809
FILING DATE: 02-PEB-1998
CLASSIPICATION: 435
                                                                       1125 ADOTSYITKTVEPTPSTEQVWIDMSETEGVFNIESVELVLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2121-135P
                                                                                                                                                                       Sequence 5, Application US/09019809
Patent No. 6143550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INPORMATION:
NAME: SYENSON, LEGNARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121.
TELECOMMUICALION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELER: 248345
INPORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
TRNGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                          -09-019-809-5
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1005 IPGMNYTSFTELTMRLQQAWNLYDLRNAIPNGDFRNGLSDWNATSDVNVQQLSDTSVLVI 1064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIVECLSDELYPNEKRMIMDAVKEAKRIVQARNILLQDTGFNRING--ENGWTGSTGIEVA 764
                                                                                                                                                    DSPASGGEVYVDKPELI PVNATPEAEEDLDVAKKA VNGLPTSKKDALQTSVTDYQVNQAA
                                                                                                                                                                                                                                                                                                                                                                                    765 EGDVLFKDRSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLKGFIGSSQDLEIKLI
                                                                                                                                                                                                                                                                                                                                                                                                    GADLANYYAQVYGVPYASFTL - - LDKNTGSGSVGGFTYSKPHTTWQVCTQNYNTIDBIPP
                                                                        475 ENEPLSRGYS-HRLSHITSYSPSKN-ASSPARYGNLPVPAWTHRSADVTNTVYSDKITQI
                                                                                                                                                                                                 593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTF---DLATIG---TAFTFSNYSDSLTVGA
                                                                                                                                    PVVKAHTLVSGTTVIKGPGFTGGNILKRTSSGPLAYTSVSVKSPLSQRYRARIRYASTTN
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APPLICANT: Wicker, Carol
APPLICANT: Warra, Kenneth E.
APPLICANT: Narra, Kenneth E.
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Brian
APPLICANT: Muller-Cohn, Judy
TITLE OF INVENTION: Toxins Active Against Pests
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Florida
COUNTRY: USA
                                ; Sequence 72, Application US/09002285; Patent No. 6369213; GENERAL INFORMATION:
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US-09-002-285-72
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241 KYTNYCETWYNTGLDRLKGTNTESWLRYHQFRREWTLVVLDVVALPPYYDVRLYPTGSNP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETPISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDF 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLTREVYTOPIVENRETSGGFCRRWSLNSDISPSEVESAVIRSPHLFDILSBIBFYTTRA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLPLNNTEYLEYWYGHSIKYKNTNASSALERNYGTITSNKIKY---YDLANKDIFQVRSL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 -FPV-SSNFMDYWSGHTLRRSYLADSAVQEDSYGLITTRATINPGVDGTNR----IEST 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSPNNQNEYEILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                         APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN RIE, JEROEN
APPLICANT: VAN AARSSEN, ROBL
TITLE OF INVENTION: NEW BACILLUS THURINGIENSIS STRAINS AND THRIR
TITLE OF INVENTION: INSECTICIDAL PROTEINS.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Palls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.7%; Score 3123; DB 4; Length 1 larity 52.3%; Pred. No. 1.9e-220; Conservative 195; Mismatches 327; Indels
                                                                                                                                                                                            COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION DATA:
RILING DATE:
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/019,809
FILING DATE: 02-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-135P
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 205-8050
VAN AUDENHOVE, KATRIEN
PEFEROEN, MARNIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
619; Conserv
                                                                                                                                                                                   COUNTRY: USA
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1066 NWNSQVSQQFTVQPRYRYVLRVTARKBGVGDGYVIIRDGANQTETLIFNICDDDTGVLSA 1125
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                                                                                                                                                                                                        826 HRANQIVRNVPDNLLPDVLPVNSCGGIDRCSBQQYVDANLALENNGENGNMSSDSHAFSF 885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVECLSDELYPNEKRMLWDAVKEAKRLVQARNILLQDTGFNRING--ENGWTGSTGIEVAE 765
                                                                                                                                                                                                                                                                                                                                                                                                                                            GDVLFKDRSLRLTSARRIDTETYPTVLYQQIDESLLKPYTRYKLKGFIGSSQDLBIKLIR 825
                                                                                           593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT----APTFSNYSDSLTVGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                946 ARKRGASEKAYYAAKOAIDRLPADYODOKLNSGVEMSDMLAAONLVOSIPYVYNDALPBI
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APPLICANT: Wicker, Carol
APPLICANT: Warvew, Kenneth E.
APPLICANT: Warvew, Kenneth E.
APPLICANT: Stockhoff, Brian
APPLICANT: Stockhoff, Lioyd & Saliwanchik
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gaineaville
STATE: Florida
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,477
FILING DATE:
FLING DATE:
PRISSIPTCATION:
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 72, Application US/09589477; Patent No. 6570005; GENERAL INPORMATION:
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ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-589-477-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 DLIDQKITDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 WNAIPLPAVNGQQVPLLSVYAQAVNIHILLLLXDASLPGBGWGFTQGBISTYYDRQLELTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MSPNNQNEYBILDASSSTSVSDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPELFGNP
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                                                                                                                                              SOFTWARE: Patentin CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/86,615
FILING DATE: 1-UL-1997
FILING DATE: 1-UL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
REGISTRATION NUMBER: 39,355
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMAT
                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1156 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TOPOLOGY: linear
1 MOLECULE TYPE: protein
US-09-002-285-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 -FPV-SSNFMDYWSGHTLRRSYLMDSAVQEDSYGLITTTRATINPGVDGTNR----IEST 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVVKAHTLVSGTTVIKGPGPTGGNILKRISSGPLAYTSVSVKSPLSQRYRARIRYASTTN 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 LRLFVTISGTRIYSINVNKTMNKGDDLTFNTFDLATIGT----APTFSNYSDSLTVGAD 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 BTPISS-STVQTGIGIVGQVLGALGVPFAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVB 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GADLANYYAQVYGVPYASPTL -- LDXNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPP 474
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                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                    Length 1156;
                                                                                                                                                                                                                                                                   tch 51.3%; Score 3100.5; DB 4; Length al Similarity 52.0%; Pred. No. 8.5e-219; 615; Conservative 196; Mismatches 330; Indels
                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNGBR: US 08/674,002
FILING DATE: 1-JUL-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
RECISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-701C1C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (352) 375-8000
TELEPAX: (352) 375-8000
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
 08/886,615
                                                                                                                                                                                   LENGTH: 1156 amino acids
APPLICATION NUMBER: US
FILING DATE: 1-JUL-1997
                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-589-477-72
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
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Search completed: June 21, 2004, 10:15:19 Job time : 31 sece